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Sequence 2088, App
Sequence 176, App
Sequence 176, App
Sequence 146, App
Sequence 149, App
Sequence 446, App
Sequence 446, App
Sequence 176, App
Sequence 149, App
Sequence 449, App
Sequence 446, App
Sequence 480, App
Sequence 480, App
Sequence 480, App
Sequence 481, App
Sequence 176, App
                  Sequence 1114, Ap. Sequence 12, Appli Sequence 1532, Appli Sequence 18, Appl Sequence 17, Appl Sequence 17, Appl Sequence 472, Appl Sequence 472, Appli Sequence 472, 
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Sequence 427, App
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Sequence 473,
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Sequence 480
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Sequence 3
Sequence 4
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APPLICANT: MCNabb, Andria
APPLICANT: McNabb, Andria
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 500
LENGTH: 577
            US-09-644-1532

US-09-873-637-11

US-09-873-637-12

US-09-873-637-12

US-09-873-637-12

US-09-873-637-12

US-09-873-637-12

US-09-873-637-12

US-09-873-637-12

US-09-873-637-12

US-09-873-637-12

US-09-873-705-146

US-09-850-716A-348

US-09-897-778-176

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US-09-897-778-146

US-09-897-778-146

US-09-897-778-146

US-09-897-778-176

US-00-117-982-148

US-10-117-982-148

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US-10-117-982-148

US-10-113-986-146

US-10-313-986-148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 500, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
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ORGANISM: Homo
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Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-LOPEL-Granz 1/USPTO spool p/USO9270437/runat 13072004_121958_10114/app_query.fasta_1.1863
-DS=rubilished_Applications_AA -OFMT=fastan -SUFFIX=rapb -MINNATCH=0.1
-LOOPEL-GO -LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=0.19
-LIGNAIS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGNAIS - MODEL-LOCAL -OUTFNT=FDC -NORM=ext -HEAPSIZE=500 -MINLEN=0
-ALIGNAIS - MODEL-GOTO-OUSR=USO9270437 @CGN 1_1 130 @runat 13072004_121958_10114
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG $\overline{SCORE} = 0 - WINT -DSPBLOCK=100
-LONGLOG -DEX TIREOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDEXT=60
-EGAPOP=6 -FGAPEXT=7 -YGAPDP=60 -YGAPEXT=60 -DELEXT=7
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'(cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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'(cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                             protein search, using frame_plus_n2p model
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Ygapop 60.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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QY 992 ATCATCATCACGCCAGAGGCCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTC 1051	515 AsnLeuThrAlaA 1232 GTCATCGTGAAAA 535 ValileValLysi 1292 GACATCCTGGCC 1255 AspileLeuAlaG	Oy 1352 CGGAGGAAG 1360 Db 575 ArgArgLys 577 RESULT 2 US-09-764-864-1114 Sequence 1114, Application US/09764864 Sequence 1118, Application US/09764864 SERNEAL INFORMATION: APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223	; CURRENT APPLICATION NUMBER: US/09/764,864 ; CURRENT FILING DATE: 2001-01-17 ; Prior application data removed - consult PALM or file wrapper ; NUMBER OF SEQ ID NOS: 1792 ; SOFTWARE: Patentin Ver. 2.0 ; SOFTWARE: Patentin Ver. 2.0 ; LENGTH: 261 ; TYPE: PRT ; ORGANIEM: Homo sapiens US-09-764-864-1114	Alignment Scores: 1.26e-197	Qy 713 TCTCACCTGATCCCTGACCTGACCTGCTAGGTCTTTTCCCAGCTTCATCCCAGC 772 B 46 SerHisbeulleProGlyLeuAsnLeuAlaAlaValGlyLeuPheProAlaSerSer 65 Qy 773 GCAGTCCGCCGCCTCCCAGCAGCGGTTACTGGGGCTGCTCCCTATAGCAG 832 Db 66 AlaValProProProProSerSerValThrGlyAlaAlaProfyrSerSerPheMetGln 85	Oy 833 GCTCCCAGCAGCAGCAGCAGCTCTTATCCCGCCCCAGGCAGTGGGCGCCATCATC 892
8.27e-241 Length: 577 261.00 Matches: 441 261.00 Conservative: 0 imilarity: 99.55 Mismatches: 0 46.61 Indels: 2 Gaps: 1 7D-5 (1-1708) x US-10-313-986-500 (1-577) 8 GCCATCATGAAGGTCCACAGTTGGAGAACCATGCCCTGAAGGTCTCCTACATC 9	98 CCCGATGAGCAGATGAGGACCTGAGAATGGGCGCCGAGGGGGCTTTGGCTCTGG 157 155 ProAspGluGlnIleAlaGlnGlyProGluAsnGlyArgArgGlyGlyPheGlySerArg 174 158 GGTCAGCCCGCAGGGCTCACCTGTGGCAGGGGCCCCAGCCAAGCAGGTG 217 158 GGTCAGCCCCAGGGCTCACCTGTGGCAGGGGGCCCCAGCCAAGCAGGTG 217 175 GlyGlnProArgGlnGlySerProValAlaAlaGlyAlaProAlaLySGlnGlnGlnVal 194 218 GACATCCCCTTGGGCCCCAGGTATGTGGTGCCATTATTGCAGAGGG 277 195 ASpIleProLeuValGeuLeuValProThrGliPl	78 GGGCCACCATCCGCAACATCACAAAACAGACCCAGGTCCAAGATAGACGTGCATAGGAAG 11	GACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTAAGTUVALLANGTAGGCGCTCTCATTAAGTUVALLANGTAGGCGCGTCTCATTAAGTUVALLANGTAGAGACGAGAAAAATCACCATGAAGAGACAAGAAAAAAAA	315 LeuGinAspieuThrieuTyrAsnProdiuArgThrileThrValLysGlyAlailediu 334 638 AATTGTTGCAGGGCCGAGCAGCAATAATGAAGAAAGTTCGGGAGGCCTATGAGAATGAT 697 135 AsnCysCysArgAlaGluGluGluIleMetLysLysValArgGluAlaTyrGluAsnAsp 354 698 GTGGCTGCCATGAGCTCTCACCTGATCCTGACCTGA	752 CTTTCCCAGCTTCATCCAGCAGTCCCGCCCTCCCAGCAGCGTTACTGGGGCTCT 811	872 CAGGCAGTGGGCGCATCATCGGCAAGAAGGGGCAGCATCAAACAGCTCTCCCGGTTT 931 [

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naturally occurring L-amino acids
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                 AlaAspGluValProLeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGly
                                                                    TCGTTGCAAGACCTTACCCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCCATC
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                                                                                                                                                                                                                                                                                       Sequence 1532, Application US/09764864
Fatent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PT223
CURRENT PAPLICATION UNMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-7
Frior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1532
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NAME/KEY: SITE

LOCATION: (127)

OTHER INFORMATION: Xaa ec;

NAME/KEY: SITE

LOCATION: (134)

COTHER INFORMATION: Xaa ec;
US-09-764-864-1532
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ORGANISM: Homo sapiens
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-764-864-1532
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US-09-873-637-2
US-09-873-637-2
; Pacture 2, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: ROSS, JGffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFRERNCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 577
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GCACCACCGGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAG
               126 AlaProProGluThrProAspSerLysValArgMetValIleIleThrGlyProProGlu
                                                                                                      CCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGG
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                                                    GCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCCAAGGAGGAGAACTTCTTTGGT
                                                                    146 AlaGlnPheLysAlaGlnGlyArglleTyrGlyLysLeuLysGluGluAsnPhePheGly
                                                                                                                                                          GTCATTGGCAAAGGTGGAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTG
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166.00
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; ORGANISM: Mus musculus
US-09-873-637-2
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Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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1253 CATTICTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAG 1312

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US-09-270-437D-5 (1-1708) x US-09-873-637-20 (1-48)
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Matches:
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ORGANISM: Mus musculus
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Best Local Similarity:
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215 HisPheTyrAlaSerGlnMetAlaGlnArgLysIleArgAspIleLeuAlaGlnValLys 234
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                                                                                                                   RESULT 5
US-09-873-637-18
US-09-873-637-18
Sequence 18, Application US/09873637
Sequence 18, Application US/09873637
Sequence 18, Application US/09873637
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: 200-05-04
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/873,637
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1313 CAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCCAGGCACGAGGAAG 1360
                                                                     235 GlnGlnHisGlnLysGlyGlnSerAsnGlnAlaGlnAlaArgArgLys 250
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ORGANISM: Mus musculus
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US-09-873-637-20
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Pred. No.:
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Percent Similarity:
Best Local Similarity:
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US-09-873-637-18
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US-09-873-637-20
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1103 ATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAAC 1162
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US-09-373-637-19

Sequence 19, Application US/09873637

Sequence 19, Application US/09873637

GENERAL INFORMATION:
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN

TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE

TITLE OF INVENTION NUMBER: US/09/873,637

CURRENT PILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 19

LENGTH: 47

TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09873637

Patent No. US2002061543A1

GENERAL INFORMATION:
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRO.BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: US/09/873,637

CURRENT APPLICATION NUMBER: US/09/873,637

CURRENT FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 17

LENGTH: 47
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Mismatches:
Indels:
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TYPE: PRT
ORGANISM: Homo
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US-10-117-982-472

US-10-117-982-472

Sequence 472, Application US/10117982

Publication No. US20030138438A1

GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.

APPLICANT: Foy, Teresa M.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Ralos, Michael D.

APPLICANT: Ralos, Michael D.

APPLICANT: Fan, Liqun

APPLICANT: Fan, Liqun

APPLICANT: Pan, Liqun

APPLICANT: WAND TONEOUSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121-455C18

CURRENT APPLICATION NUMBER: US/10/117,982

CURRENT FILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 484

SEQ ID NO 472

ELENCTH: 70

TYPE: PRT
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; ORGANISM: Mus musculus US-09-873-637-19
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US-10-117-982-472
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Best Local Similarity:
Query Match:
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RESULT 10

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US-10-408-765A-2088
US-10-408-765A-2088
US-10-408-765A-2088
Sequence 2088, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Bing
APPLICANT: Ghosh, Bradford W.
APPLICANT: Glason, 
Sequence 472, Application US/10313986

Publication No. US20030236209A1

GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF SINVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF SINVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/10/313,986

CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 472
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ORGANISM: Homo sapiens
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Query Match:
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McNeill, Patricia D.
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CRGANISM: Homo sapiens
US-09-850-716A-176
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Pred. No.:
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                                          254 GTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCGAG 313
                                                               50 ValGlyAlaIleIleGlyLysGluGlyAlaThrIleArgAsnIleThrLysGlnThrGln 69
                                                                                                                                                                                                                                                                                           APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Rangur, Chaitaely S.
APPLICANT: Bangur, Chaitaely S.
APPLICANT: Bangur, Chaitaely S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wowelll, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: None: 11, 455014
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE REPERBNCE: 21012.455014
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SEQ ID NO 176
IEBNGTH: 579
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                                                                                                                       314 TCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAA 361
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US-09-270-437D-5 (1-1708) x US-10-408-765A-2088 (1-422)
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US-09-735-705-348
US-09-735-705-348
Sequence 348, Application US/09735705
Patent No. US2002052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bengur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                                       Sequence 176, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
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Skeiky, Yasir A.W.
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US-09-735-705-176
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US-09-735-705-176
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
; CURRENY APPLICATION NUMBER: US/09/735,705
; CURRENY TILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSEQ for Windows Version 3.0
; SOFTWARE: FR
LENGTH: 579
; TYPE: RRT
CRGANISM: Homo sapiens
US-09-735-705-348
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US-09-850-7164-176
| Sacure 176, Application US/09850716A
| Patent No. US20020115199A1
| GENERAL INFORMATION:
| APPLICANT: Kalos, Michael D.
| APPLICANT: Retter, Marc W.
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER |
| TITLE REPERBYCE: 210121.455015 |
| CURRENT FILING DATE: 2001-05-07 |
| NUMBER OF SEQ ID NOS: 440 |
| SEQ ID NO 176 |
| SEQ ID NO 176 |
| LENGTH: 579 |
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US-09-850-716A-348

US-09-850-716A-348

Sequence 348, Application US/09850716A

Sequence 10. US2020115139A1

GENERAL INFORMATION:

APPLICANT: RACEAL, Machael D.

APPLICANT: RACEAL, MACHAIL D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIGGNOSIS OF LUNG CANCER

TITLE OF INVENTION: AND DIGGNOSIS OF LUNG CANCER

CURRENT PILING DATE: 2001-05-07

NUMBER: 05-07

SEQ ID NO 349

SEQ ID NO 340

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O00425 homo sapien
Q8c2j9 mus musculu
Q9cpn8 mus musculu
Q9pw80 brachydanio
Q9y6m1 homo sapien
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Q9truo brachydanio
Q9truo brachydanio
Q9uin6 homo sapien
Q9uin7 homo sapien
Q9uin7 homo sapien
Q9uin8 homo sapien
Q9nrh4 homo sapien
Q9nrh4 homo sapien
Q9nrh9 homo sapien
Q9nrh9 homo sapien
Q9nrh6 homo sapien
Q9sigus homo sapien
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Q8sigus qallus qallus
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Q97zk6 streptococc
Q8cyy6 streptococc
Q9gmuy macaca fasc
Q93fz2 pectobacter
                                   088477 mus musculu
Q80us9 mus musculu
Q42254 galllus gall
O73932 xenopus lae
O57526 xenopus lae
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EDM T., Singer R.H., Bassell G.J.;

Molecular interactions between rZBP1 and b-actin zipcode required for transport of mRNA and stimulation of spine growth.";

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF541940; AAO16210.1;

GO, GO:0003676; F:nucleic acid binding; IEA.

InterPro; IPR004088; KH_Cype_1.

InterPro; IPR004088; KH_Cype_1.

InterPro; IPR005084; RNA_rec_mot.

Pfam; PF00013; KH; 4.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
B-actin zipcode binding protein 1.
Rattus norvegicus (Rat).
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCB_TAXID=10116;
                  08BRH1
088477
088477
084254
074255
057526
000425
09CENB
09PWB0
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0872V2
0872V2
09NRH5
09NRH7
09NRB5
09NRB6
09NRB6
086Z04
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086Z04
081ZU4
081ZU4
081ZU4
091ZU4
091ZU5
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                              - protein search, using frame_plus_n2p model
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sp_vertebrate:*
sp_unclassified:*
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sp_fung::*
sp_human:*
sp_nammal:*
sp_mammal:*
sp_organelle:*
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Match Length DB
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Ygapop 60.0 , Y
Fgapop 6.0 , F
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GTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAA 1144
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                Euteleostomi;
Homo.
                                                                                Ioannidis P., Trangas T., Dimitriadis E., Samiotaki M., Panoutsakopoulos G., Kyriazoglou I., Voutzoulias S., Tsiapalis Kittas C., Agnantis N., Pandis N., Bctopic expression of a Kaldomain containing protein, highly homologous to both human IMP-1 and mouse CRD-BP, in benign and
                                                                                                                                                 malignatum mesenchymal tumors.;

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-!-SIMILABITY: CONTAINS 4 KH DOMAINS.

EMBL; AF198254; AAF3703.1; -.

InterPro; IPR004089; KH, dom.

InterPro; IPR004089; KH, dom.

InterPro; IPR004089; KH, dom.

EMARY; SM00350; KH, dom.

EMARY; SM00322; KH, dom.

EMBL; FSS0084; KR, TYPE 1, dom.
                Craniata, Vertebrata; E
Catarrhini, Hominidae;
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Mismatches:
Indels:
Gaps:
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              Chordata;
Primates;
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100.00%
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    sapiens (Human)
  Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local Similarity:
Query Match:
DB:
                                                                    SEQUENCE FROM N.A.
                                           NCBI_TaxID=9606;
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Pred. No.:
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Pfam; PF00076; rrm; 2.
SWART; SM0322; KH; 4.
SWART; SM0360; RRM; 2.
PROSITE; PS50084; KH TYPE_1; 4.
PROSITE; PS50102; KRM; 2.
SEQUENCE 577 AA; 63436 MW; 0647676128FBD1EE CRC64;
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                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=94179348; PubMed=8132663;
Prokipcak R.D., Herrick D.J., Ross J.;
Prokipcak and properties of a protein that binds to the C-terminal
"Purification of human c-myc mRNA.";
J. Biol. Chem. 269:9261-9269(1994).
                                                                                                                314 SerbeuGlnAspLeuThrbeuTyrAsnProGluArgThrIleThrValLysGlyAlaile
274 AlaAspGluValProLeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGly
                                                                                               575 TCGTTGCAAGACCTTACCCCTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATC
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MEDLINE=21085660; PubMed=11217851;
Mawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDLINE=9732234; PubMed=9178888;
Leeds P., Kren B.T., Boylan J.M., Betz N.A., Steer C.J.,
Gruppuso P.A., Ross J.;
"Developmental regulation of CRD-BP, an RNA-binding protein is tabilizes c-myc mRNA in vitro.";
Oncogene 14:1279-1286(1997).
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Fleisig A.J.; Bubmitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=92217743; PubMed=1559612;
Bernstein P.L., Herrick D.J., Prokipcak R.D., Ross J.;
"Control of c-myc mRNA half-life in vitro by a protein binding to a coding region stability determinant.";
Genes Dev. 6:642-654(1992).
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Coding region determinant binding protein.
IGF2BP1 OR CRDBP.
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Mol. Cell. Biol. 14:2119-2128(1994).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Insulin-like growth factor 2.
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                                                                                                                                                                                                                                                                                                                                                                                                 GCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGC 514
                                                                                                                                                                                                                                                                                                                                                                                                         515 AAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCC 574
                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGTTGCAAGACCTTACCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATC 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 GAGAATTGTTGCAGGCCGAGCAGGAAATAATGAAGAAGTTCGGGAGGCCTATGAGAAT 694
                                                                                                                                                                                                                                                                                           GTGGACATCCCCCTTCGGCTCCTGGTGCCCAGTATGTGGGTGCCATTATTGGCAAG
                                                                                                                                                                                                                                                                                                    194 ValAspileProLeuArgLeuLeuValProThrGlnTyrValGlyAlaileileGlyLys
                                                                                                                                                                                                                                                                                                                           GAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG
                                                                                                                                                                                                              577 AA; 63450 MW; EFBBIAF2FF9F0344 CRC64;
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                               (1-577)
                                                                                                                                                                       Pfam; PF00013; KH; 4.

Pfam; PF00076; rrm; 2.

SMART; SM00322; KH; 4.

SMART; SM00360; RRM; 2.

PROSITE; PS50004; KH TYPE 1; 4.

PROSITE; PS50102; RRM; 2.
                                                                                                                                                                                                                                                                              US-09-270-437D-5 (1-1708) x 088477
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166.00
100.00%
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Best Local Similarity:
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Pred. No.:
Score:
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                                                                                                                                                                                                               SEQUENCE
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RAY SEQUENCE FROM N.A.

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SEQUENCE TO N.A.

SEQUENCE TO STRAIN=129/Sv. x 129/Sv.-CP; TISSUE=Embryonic stem cells;

KANDELNEE=238825; PubMed=1247932;

RAY Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RAY Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RAY Hopkins R.F., Jordan H., More T.T., Mars J., Haiat N. K.,

RAY Hopkins R.F., Jordan H., More T.T., Mars J., Haiat N. K.,

RAY Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Haiat N. K.,

RAY Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RAY Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RAY Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RAY Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RAY Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RAY Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

RAY Whiting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

RAY Mitting M., Madan A., Young A.C., Shevchenko Y., Bulterfield Y.S.,

RAY Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RAY Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RAY Generation and initial analysis of more than 15,000 full-length human
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334 GluasnCysCysArgalaGluGlnGluIleMetLysLysValargGluAlaTyrGluAsn 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Strausberg R.;
Strausberg R.;
Submittee (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051679; AAH5199.1;
GO; GO:0030576; F:nucleic acid binding; IEA.
R. InterPro; IPR004089; KH dom.
R. InterPro; IPR004089; KH ± type 1.
R. InterPro; IPR004089; KH; 4.
R. InterPro; IPR004089; KH; 4.
R. InterPro; IPR004089; KH; 4.
R. SMART; SM00320; KH; 4.
R. SMART; SM00320; KH; 4.
R. SMART; SM00320; RRM; 2.
R. PROSITE; PSS0084; KH TYPE 1; 4.
R. PROSITE; PSS0084; KH TYPE 1; 4.
SMART; SM00320; RRM; 2.
R. PROSITE; PSS0084; KH TYPE 1; 4.
SMART; SM00320; RRM; 2.
R. PROSITE; PSS0084; KH TYPE 1; 4.
SMART; SM00320; RRM; 2.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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983 CGTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTAT 1042
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                                                              1115 GCATCAGCAGCTGGCCGGGTCATTGGCAAAAGGTGGAAAAACGGTGAAACGAGTTGCAGAAT 1174
                                                                                                    465 ArgMetValileIleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglleTyr 484
475 GluGluAsnPhePheGlyProLysGluGluValLysLeuGluThrHisIleArgValPro 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 GlyLysLeuLysGluGluAsnPhePheGlyProLysGluGluValLysLeuGluThrHis
                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VG1 RNA binding protein variant D.
VG1 RNA binding protein variant D.
Eukaryots, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopus.
                                                                                                                                                                                               1175 TTGACGCCAGCTGATGGTACCAAGAGACCAGACCCCTGATGAGAAC 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98228351; PubMed=9560341;
MEDLINE=98228351; PubMed=9560341;
MEDLINE=98228351; PubMed=9560341;
Medline=98228351; PubMed=9560341;
Medline=98228351; PubMed=9560341;
Medline=9822831; PubMed=9560341;
Medline=9822831; Medline=98231; Medline=98331; Medline=983
                                                                                                                                                                                                                                  515 LeuThrAlaAlaGluValValValProArgAspGlnThrProAspGluAsn 531
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0 0 0 0 0
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PROSITE; PS50102; RRM; 2.
SEQUENCE 594 AA; 65643 MW· F
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                TTGACGGCAGCTGAGGTGGTAGTACCAAGAGCCGGACCCCTGATGAGAACGACCAGGTC 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGAC 1294
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WEDUINE=97220007; PubMed=9121465;
REDIINE=97220007; PubMed=9121465;
REDIINE=97220007; PubMed=9121465;
REDIINE=97220007; PubMed=9121465;
REDIINES A.F. Oleynlikov Y.S. Kislauskis E.H., Taneja K.L., Singer R.H.;
R. "Characterization of a beta-actin mRNA zipcode-binding protein.";
R. "Characterization of a beta-actin mRNA zipcode-binding zipcode-bin
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                                                                                                                                                                                                                                  455 IleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglleTyrGlyLysLeuLys 474
                                                                                                                                                                                                                                                                                                                                                                                              535
456 IleThrGlyProFroGluAlaGlnPheLysAlaGlnGlyArglleTyrGlyLysLeuLys 475
                                                                                                           GCATCAGCAGCTGGCCGGGTCATTGGCAAAAGGTGGAAAAACGGTGAAACGAGTTGCAGAAT
                                                                                                                                                                                                                                                                                                                                                                      Zipcode-binding protein.
ZBP1.
Gallus gallus (Chicken).
Brukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Indels:
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Best Local Similarity:
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NCBI_TaxID=9031;
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Pred. No.:
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                                                                                                                             476
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042254;
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042254
2AC 042234
DT 01-30
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.72e-28
36.00
100.00%
100.00%
6.43%
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                                                                                     SEQUENCE FROM N.A.
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Best Local Similarity:
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                               TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGF2BP3.
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Q8C2J9
   SON REPRESENTATION OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 ArgMetValileIleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArgIleTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
KH domain-containing transcription factor B3.
KH domain-aevis (African clawed frog).
Eukaryota, Metazoa; Ghordata, Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=92249652; PubMed=1577195;
Pfaff S.L., Taylor W.L.;
"Characterization of a Xenopus oocyte factor that binds to a developmentally regulated cis-element in the TFIIIA gene.";
Dev. Biol. 151:306-316(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Griffin D., Taylor W.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Havin L., Git A., Elisha Z., Oberman F., Yaniv K.,
Havin L., Git A., Elisha Z., Oberman F., Yaniv K.,
Pressman Schwartz S., Standart N.M., Yisraeli J.K.;
Genes Dev. O:0-0(1998).
--- SIMILARITY: CONTAINS 4 KH DOMAINS.
EMBL, AF0642353 AAB94957.1; --
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004087; KH dom.
InterPro; IPR004089; KH type 1.
InterPro; IPR004089; KH type 1.
InterPro; IPR004089; KH type 1.
InterPro; IPR004089; KH 4.
SPÉam; PF00013; KH; 4.
SWART; SM00322; KH; 4.
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PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM RNP_1; PALSE_NEG.
SEQUENCE 593 AA; 65385 MW; 5A5AB4B4A1D55DF7 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative RNA binding protein KOC (KOC).
KOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    579 AA
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                             PRT;
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38.00
100.00%
100.00%
6.79%
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                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
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057526
                                DDT TENDER TO DESCRIPTION OF THE PROPERTY OF T
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254 GTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAG 313
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MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

The FANTOM COnsortium,

The FANTOM Consortium,

The RANDOM Consortium;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length, cDNAs.";

Nature 420:563-573 (2002).

MALUS 420:563-573 (2002).

MGD; MGI:1890359; Igf2bp3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Wouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerlysileAspValHisArgLysGluAsnAlaGlyAlaAlaGluLys 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 TCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAA 361
                                                                                         AL.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Insulin-like growth factor 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Mueller-Pillasch F., Lacher U., Wallrapp C., Oncogene 0:0-0(0).
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227
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Q9PW80
ID Q9PW8(
AC Q9PW8(
DT 01-MA)
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RECORDENCE FROW N., Stinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Adachi J., Fukuda S., Arawawa T., Bara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., Arawawa T., Salto T., Okazaki Y., Golobori T., Bono H., Kasiwawa T., Salto R., Ashburner M., Betalov S., Gasvant T., Radota K., Matsuda H., Ashburner M., Betalov S., Gasvant T., Radota K., Matsuda H., Shinaki R., Cochiwa H., Radota K., Matsudi H., Stauki R., Tomita M., Wagner L., Washio T., Rasai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Barak J., Boffelli D., Bolinga N., Carninci P., de Bonaldo M.F., Rabar S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Loyons P., Marchioni L., Mashima J., Machina I., Mondone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Loyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F., Ruyashizani Y., Toyo-oka K., Wang K.H., Weitz C., Wilming I., Mashian Y., Kawaji H., Kohteuki S., Hassahan Y., Kawaji H., Kohteuki S., Hassahizani Y., Rawaji H., Kohteuki S., Hassahizani Y., Rawaji H., Kohteuki S., Hassahizani Y., Rawaji H., Kabetuki S., Marshawali K., Hassagawa Y., Kawaji H., Kabetuki S., Hassahizani Y., Rawaji H., Kabetuki Y., Rawaji H., Kabetuki R., Hassahizani Y., Rawaji H., Kabetuki Y., Hassahizani K., Hassahizan
                                                                                                                                                                                                                                                                                                                                                                                                                    ValGlyAlaileileGlyLysGluGlyAlaThrileArgAsnileThrLysGlnThrGln 226
                                                                                                                                                                                                                                                                                                                                                                                             GTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCAG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 12, Last sequence update)
10 days embryo CDNA, RIKEN full-length enriched library,
clone: 2610058B18, full insert sequence (Igf2 mRNA-binding protein 3)
[Insulin-like growth factor 2, binding protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mori H., Sakakibara S., Imai T., Nakamura Y., Iijima T., Suzuki A.,
Yuasa Y., Takeda M., Okano H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                 InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
InterPro; IPR000508; KH_type_1.
Pfam; PF00013; KH; 4.
Pfam; PF00013; KH; 4.
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
PROSTITE; PS50084; KH TYPE_1; 4.
PROSTITE; PS50084; KH TYPE_1; 4.
SROJUENCE 579 AA; 63551 MW; 937E601A95D06B77 CRC64;
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Matches:
Conservative:
Mismatches:
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GO; GO:0003676; F:nucleic acid binding; IEA.
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30.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                      5.36%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                 Alignment Scores:
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DB:
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                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                     Score:
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain, and Olfactory epithelium;

MEDINE=2238825; PubMed=1247793;

Altausherg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altachul S.P., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

Altachul S.P., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Altachul S.P., Zeeberg B., Moore T., Max S.I., Wang J., Haieh F.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKernan K.J., Malled J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"M. Gorneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Expression of mouse igf2 mRNA-binding protein 3 and its implications for the developing central nervous system."; J. Neurosci. Res. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stransberg R.;
Stransberg R.;
Stransberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SINLIARITY: CONTAINS 4 KH DOMAINS.
EMBL; AKO11699; BARB27779.1; -.
EMBL; ARO46173; BAB19755.1; -.
EMBL; BC045138; AAH45082.1; -.
EMBL; BC045138; AAH45082.1; -.
EMBL; MGJ189082; AAH45082.1; -.
MGD; MGJ189082; Agf2bp3.
GO; GO:0003676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain, and Olfactory epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00013; KH; 4.
Pfam; PF00013; KH; 4.
SWART; SM0032; KH; 4.
SWART; SM00360; RRM; 2.
PROSTIE; PS501084; KH TYPE_1; 4.
SEQUENCE 579 AA; 63574 MW; CABD9A4355B392B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerLysileAspValHisArgLysGluAsn 236
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InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_top.
InterPro; IPR00504; RNA_rec_mo
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01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
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Best Local Similarity:
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277 ProLeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArg 296

527 AACCTGAAGAAG 538

à

PRT;

PRELIMINARY;

Q9Y6M1

RESULT 13

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TASSUBBLEDGLY;

RA KLAUSBET R. S. PubMed=12477932;

KLAUSBET R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carannor T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carannor P.D., Mullahy S.J.,

RA S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzrathe P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Ray Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length human

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Vgl RNA binding protein (Decapentaplegic and Vg-related 1, RNA binding
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Zhang Q., Yaniv K., Oberman F., Wolke U., Git A., Fromer M.,
Taylor W., Meyer D., Standart N., Raz E., Yisraeli J.K.,
"Vgl RBP intracellular distribution and evolutionarily conserved
expression suggest multiple roles during development.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=BB: STRAIN=BB: STRAIN=BB: STRAIN=BB: Strainsberg R.; Strainsberg G.; Strainsterd (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF00076; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM0030; RRH; 2.
PROSITE; PS50084; KH TYPE 1; 4.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50102; RRM; 2.
                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
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EMBL, AF161270, AAD55610.1, -
EMBL, BC045873, AAH5873.1, -
EMBL, BC05876, F:mucleic acid binding; IEA.
InterPro; IPR004087, KH.dom.
InterPro; IPR004088, KH.type.1.
InterPro; IPR00504, RNA_rec_mot.
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RAY MEDLINE-99207072; PubMed=10190901,

RAY Chang U.Y., Chan E.K., Peng X.X., Tan E.M.;

Zhang U.Y., Chan E.K., Peng X.X., Tan E.M.;

The Movel Cytoplasmic protein with RNA-binding motifs is an autoantigen

RT in human hepatocellular carcinoma.";

J. Exp. Med. 18:1101-1110(1999).

-: SIMILARITY: COUNTRINS 4 KH DOMAINS.

-: SIMILARITY: COUNTRINS 7 COUNTRINS 600 CG:0005737; C:Cytoplasm; TAS.

GO: GO:0007373; PRAD MISSO 1.1.

GO: GO:0007373; PRAD MISSO 2.1.

GO: GO:0007373; PRAD MISSO 3.1.

ROY GO:0007373; PRAD MISSO 3.1.

ROY GO:0007374; PRAD MISSO 3.1.

ROY GO:0007374; PRAD MISSO 3.1.

ROY GO:0007375; PRAD MISSO 3.1.

ROY GO:0007375; PRAD MISSO 3.1.

ROY GO:00076; RNA Trec_mot.

REAT: PRO0013; KH; 4.

SWART; SM0322; KH; 4.

ROY SESSO 3.1.

ROY FROM SESSO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 ArgMetValllelleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglle 449
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Xu C.S., Li W.Q., Li Y.C., Yang K.J., Yan H.M., Chang C.F., Zhao L.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            556 AA; 61842 MW; 1EDEFB100443DDC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatocellular carcinoma autoantigen.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                              Homo sapiens (Human).
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                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Q7TP50
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582 40000 24

Length:
Matches:
Conservative:
Mismatches:

2.3e-15 24.00 100.00% 100.00% 4.29%

Percent Similarity: Best Local Similarity:

Query Match:

indels: Gaps:

US-09-270-437D-5 (1-1708) x Q9PW80 (1-582)

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RECUENCE FROM N.A.

SEQUENCE FROM N.A.

RC STRAIN-657BL/6; TISSUE-Brain;

RX MIDINE-22386257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Waxs I., Wang J., Haieh F.,

RA Hopkins R.F., Jordan H., Moore T., Waxs I., Wang J., Haieh F.,

RA Diacchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Jodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Munny D.M., Schergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Shevchenny C.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

RA Jones S.J., Marra M.A.,

RA Jones S.J., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
Ma H., Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
"Liver regeneration after PH.";
Subnitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY328199; AAP928600.1; -.
SEQUENCE 169 AA; 17743 MW; 19BF6295C1000CBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Muscaryotas, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinuse, MuscullaraxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054552; AAH5552.1; -.
Hypothetical protein:
SEQUENCE 545 AA; 59679 MW; 88DD35FF30DF3091 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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2.68%
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16.00
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Pred. No.:
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Pred. No.:
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US-09-270-437D-5 (1-1708) x Q7TQF9 (1-545)
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494 TTTGTAGGGCGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAG 538

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Search completed: July 13, 2004, 12:34:38 Job time : 100 secs

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Sequence 20, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 170, Appli Sequence 170, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 33, Appli Sequence 34, Appli Sequence 34, Appli Sequence 2996, Appli Sequence 34, Appli Sequence 441, Appli Sequence 6421, Appli

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APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Grayer, Elke
APPLICANT: Gld, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CCAGTIGGAGAACCATGCCCTGAAGGCTCCCTACATCCCCGATGAGCAGATAGCACAGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CCAGTIGGAGAACCAIGCCCIGAAGGICTCCIACAICCCCGAIGAGCAGAIAGCACAGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGANGCTGCCGCACCGCCCCAGTTTACCCCGGGAGCCATCATGAAGCTGAATGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GCCCACCCAGTATGTGGGTGCCATTATTGGCAAGGAGGGGGCCACCATCCGCAACATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGGACGCTGCCGCACCGCCCCCAGTTTACCCCGGGGAGCCATCATGAAGCTGAATGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TGTGGCAGCGGGGCCCCCAGCCAAGCAGCAGCAAGTGGACATCCCCCTTCGGCTCCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 1708;
US-09-528-709-20
US-08-528-705-20
US-08-695-737-1
US-08-4480-145-1
US-08-340-428B-1
PCT-US93-07306-1
US-08-956-171E-170
5180808-1
US-09-479-128-1
US-09-479-128-1
US-09-479-128-1
US-09-103-840A-1
US-09-261-855-33
US-09-261-855-33
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US-09-51-858-34
US-09-51-858-34
US-09-134-000C-3161
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Pred. No. 0;
; Mismatches
                                                                                                                                                                                                                   ALIGNMENTS
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Sequence 5, Sequence 5, Setent No. 6297364

; Patent No. 6297364

; GENERAL INFORMATION:
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100.0%; Pr
tive 0;
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44115
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Best Local Similarity 100.
Matches 1708, Conservative
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189
312
462
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   1708
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Sequence 7, Appli
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Sequence 38, Appl
Sequence 38, Appl
Sequence 347, Appl
Sequence 347, Appl
Sequence 177, Appl
Sequence 175, Appl
Sequence 286, Appl
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(without alignments)
7073.553 Million cell updates/sec
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                                                                                                                                          1 agggacgctgccgcaccgcc.....atttccttcaggttttaaaa 1708
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Compugen Ltd.
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US-09-89-651-5
US-09-89-651-5
US-09-261-855-18
US-09-261-855-38
US-09-261-855-38
US-09-643-597-347
US-09-643-597-347
US-09-643-597-347
US-09-643-597-347
US-09-601-709-4
US-09-709-709-4
US-09-709-709-7
US-09-709-709-7
US-09-709-7
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                             682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
            GenCore version
Copyright (c) 1993 - 2004
                                                       nucleic search, using sw model
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                                                                                                                                                                         Gapop_60.0 , Gapext 60.0
                                                                          July 13, 2004, 23:27:48
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seq length: 200000000
                                                                                                                     US-09-270-437D-5
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	Oy 1597 AGGCAAGGCACTTTAAACGTGGATTGTTTAAAGAAGGTCTCCAGGCCCCACCAAGAGG 1656	m m	CANT: 18ang, 20 CANT: 5cockert CANT: 5cockert CANT: CANT: CANT: CANT: CANT: 01d, L1C CANT: 01c INVENTION: 0F INVENTION:	FILE REFERENCE: LUD 509/899,651 CURRENT APPLICATION NUMBER: US/09/899,651 CURRENT FILING DATE: 2001-07-06 FRIOR PEPLICATION NUMBER: US/09/061,709 PRIOR FILING DATE: 1998-04-17 NUMBER OF SEQ ID NOS: 8	FO-0	Query Match 97.9%; Score 1672; DB 4; Length 1946; Best Local Similarity 100.0%; Pred. No. 0; Matches 1672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 37 AGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTTCCTACAT 96	QY 97 CCCCGATGAGCAGAGACCTCAGAAATGGGCGCCGAGGGGCTTTGGCTCTCG 156 Db 335 CCCCGATGAGCAGATAGGACCTGAGAATGGGCGCCGAGGGGCTTTGGCTCTCG 394	0y 157 GGGTCAGCCCGCCAGGGCTCACCTGTGGCAGCGGGGGGCCCCAGCCAG	9y 217 GGACATCCCCTTCGGCTCCTGGTGCCCACCCACTATGTGGCTGCCTTATTGGCAAGGA 276	QY 277 GGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGGAA 336
515 GGGGGCCACCATCCGCAAAACCGAGCCCAGTCCAAGATAGACGTGCTAAGGAA 574	17 GGAAGGACGGAACCTGAAGAAGGTAGAGGTACCGAGACAAAATCACCAT	637 GAATTGTTGCAGGCCCGAGCAGAATAATGAAGAAAGTTCGGGAGGCCTATGAGAATGA 696	757 CCCAGCTTCATCCAGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCCTA 816		7 CCTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGA	1057 GGAGAACTICTITGGTCCCAAGGAGAGAGAGAGGCTGGAGACCCACATACGTGTGCCAGC 1116 	1117 ATCAGCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAACGGTGAACGAGTTGCAGAATTT 1176 	1177 GACGGCAGCTGAGGTGGTAGCAGACCAGACCCCTGATGAGAACGACCAGGTCAT 1236 	1237 CGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACCT 1296 	1297 CCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGACAGAGTAACCAGGCCCAGGCACGGAG 1356 	1357 GAAGTGACCAGCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACGGCAGAAATCGAGA 1416

1417 GTGTGCTCCCGGCAGGCCTGAGAATGAGTGGGAACNTGGGCCGGCTG 146		<pre></pre>	RESULT 6 US-09-261-855-38/C J Sequence 38, Application US/09261855A J Sequence 38, Application US/09261855A J Ratent No. 6255055 GENERAL INFORMATION: J TILLE OF INVENTION: (CRD-BP) TILLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE TILLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE CURRENT APPLICATION NUMBER: US/09/261,855A CURRENT FILING DATE: 1999-03-03 NUMBER OF SEQ ID NOS: 46 SSETURARE: PATENTIN VEY: 2.0 SSETURENT DATE: PATENTIN VEY: 2.0	JENGIN 24 JENGIN 24 ORGANISM: Artificial Sequence PEATURE: OTHER INFORMATION: Oligonuclectide primer JOS-09-261-855-38 Query Match Best Local Similarity 100.0%; Pred. No. 0.032; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	637 GAATTOTTGCAGGCCGAGCAGGAATAATGAAGAAGTTCGGGAGGCCTATGAGAATGA 875 GAATTOTTGCAGGCCGAGCAGGAATAATGAAGAAAGTTCGGGAGGCCTATGAGAATGA 697 TGTGGCTGCCATGAGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGCTGTAGGTCTTTT 	Oy 877 AGTGGGCGCCATCATCATGGCAAGAGGGGAACACATCTCCCGGTTTGCCAG 936 Db 11115 AGTGGCGCATCATCGAGAAGGGCACCACATCAACAGCTCTCCCGGTTTGCCAG 1116 AGTGGCCGATCATCGAGAAGGCCACCACCACACATCAACACTCCCGGTTTGCCAG 1174 Qy 937 CGCCTCCATCAAGATTGCACCACCCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCAT 996 Db 1175 CGCCTCCATCAAGATTGCACCACCCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCAT 1234 Qy 997 CACTGGACCGCCAAGAGCTCAAGGCTCAAGAACACTCAAGGA 1056 Db 1235 CACTGGACCGCCAAGAGCCCAATTCAAGGCTCAAGAAACTTATGGCAAACTCAAGGA 1056 Db 1235 CACTGGACCGCCAAGAACACCCCAATTCAAGGCTCAAGAAATCTATGGCAAACTCAAAGA 1294		

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APPLICANT: Ward, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFREENCE: 210121.455C9
CURRENT APPLICATION WUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: PASKSEQ for Windows Version 3.0
LENGTH: 1740
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4;
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                                                                       GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liquin
APPLICANT: Fan, Liquin
APPLICANT: Fan, Liquin
APPLICANT: Fan, Liquin
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Compounds and METHODS FOR THERAPY
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Pred. No. 4;
iive 0; Mismatches
                US-09-542-615A-347
; Sequence 347, Application US/09542615A
; Patent No. 6518256
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US-09-606-421B-347
; Sequence 347, Application US/09606421B
; Patent No. 6531315
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APPLICANT: Wang, Tongrong
APPLICANT: Fan, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosker, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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CRGANISM: Homo sapiens
US-09-606-421B-347
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ORGANISM: Homo sapiens
US-09-542-615A-347
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Best Local Similarity
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SEQ ID NO 347
LENGTH: 1740
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APPLICANT: McNeall, Particias D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210.021.455CII.
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: US/09.08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastsEc for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2%; Score 20; DB 4; Length 1740;
100.0%; Pred. No. 4;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.1;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Oligonucleotide primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1178 ACGCCAGCTGAGGTGGTAGTACC 1200
508 CATTGGCAAGGAAGGACGGAACCT 531
                                       24 CATTGGCAAGGAAGGACGGAACCT 1
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Patent No. 6426072
GENERAL INFORMATION:
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Seguence
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Matches 23; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 20; Conserva
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APPLICANT:
APPLICANT:
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APPLICANT: Fan, Linguin
APPLICANT: Fan, Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Ti, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Mederson, Robert A.
APPLICANT: MONOFILL Patricia D.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILLS REFERENCE: 210121.455C11
CURRENT FILLNG DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOUTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 175
LENGTH: 4181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: UNGUE
LOCATION: (3940)
OCHER INFORMATION: n=A,T,C or G
NAME/KEY: UNGUE
LOCATION: (3968)
OCHER INFORMATION: n=A,T,C or G
NAME/KEY: UNGUE
LOCATION: (3974)
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LOCATION: (3347)
NAME/KEY: unsure
LOCATION: (3502)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3506)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3506)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3520)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3520)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3538)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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NAME/KEY: unsure
LOCATION: (4036)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4056)
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LOCATION: (3646)
OTHER INFORMATION: n=A,T,C or
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OTHER INFORMATION: n=A,T,C or
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                     Tongtong
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ORGANISM: Homo sapiens
Wang, ic
Liqun
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) LOCATION: (4088)
) OTHER INFORMATION: IN
) NAME/KEY: unsure
) LOCATION: (4115)
) OTHER INFORMATION: IN
US-09-643-597-175
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LOCATION: (4080)
OTHER INFORMATION:
                            FAREIL NO. '2575730';

APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Tang, Solam
APPLICANT: Tang, Solam
APPLICANT: Tang, Solam
APPLICANT: Tang, Solam
APPLICANT: Muth, Alexander
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
ILENGTH: 4159
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Patent No. 6276756

GENERAL INFORMATION:
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Stockert, Elke
APPLICANT: Jold, Lloyd J.
TITLE OF INVENTION: Absociated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: Antigen, The Antigens
FILE REFERENCE: LUD 5538
CURRENT FILICATION NUMBER: US/09/061,709
PRIOR APPLICATION NUMBER: US/09/061,709
PRIOR PELICATION NUMBER: US/09/061,709
PRIOR FILING DATE: 1998-04-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.2%; Score 20; DB 3; Length 4159; Best Local Similarity 100.0%; Pred. No. 4.2; Matches 20; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.2;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1019 TTCAAGGCTCAGGGAAGAAT 1038
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US-09-643-597-175
IS-09-643-597-175
Sequence 175, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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US-09-899-651-4
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US-09-899-651-4
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    DB 4; Length 4181; 4.2;
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Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                               0; Indels
                                                                                                                                                                                                                                                                                         RESULT 14
US-09-480-884A-175
Sequence 175, Application US/09480884A
Fatent No. 6482597
GENERAL INFORMATION:
FAPLICANT: Wang, Tongtong
APPLICANT: Hosken, Nancy A.
FAPLICANT: Acalos, Michael D.
APPLICANT: Acalos, Michael D.
APPLICANT: Acalos, Michael D.
FILE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS OF LUNG CANCER
FILE REFERENCE: 210121-455C6
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 175
LENGTH 4181
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US-09-542-615A-175
Sequence 175, Application US/09542615A
Patent No. 651826
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.4556
CURRENT FILING DATE: 2000-04-14
NUMBER OF SUG ID NOS: 350
SOFTWARE FERSENCE FEASTERE FASTERE FEASTERE FASTERE FEASTERE FASTERE FOR SUCH AND SUGFFARE FASTERE FAS
Query Match 1.2%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 4.2 Matches 20; Conservative 0; Mismatches
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; LOCATION: (1)...(4181)
; OTHER INFORMATION: n=A,T,C or G
US-09-480-884A-I75
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LOCATION: (3347)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3502)
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ORGANISM: Homo sapiens
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LENGTH: 4181
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GRSB_BACBR
RXR1_PIG
RXR1_PIG
RXR1_HUMAN
RM33_VIBCH
RM33_VIBCH
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ALIGNMENTS

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	copyright (c) 1993 - 2004 Compugen Ltd.	O	21	00	1.4	5037
		U	22	ω	1.4	5038
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i		υ	25	7	1,3	86
Kun on:	July 13, 2004, 12:14:48 ; Search time 19.5 Seconds	O	. 26	7	1.3	86
	(without alignments)	υ	27	7	1.3	101
	9121.623 Million cell updates/sec	U	28	7	1.3	110
1		υ	29	7	1.3	113
Title:	US-09-270-437D-5	υ	30	7	1.3	114
Pertect score:	260	υ	31	7	1.3	124
sednence:	l agggacgctgccgcaccgccatttccttcaggttttaaaa 1708	U	32	7	1.3	124
		υ	33	7	1.3	136
scoring table:	OSITO		34	7	1.2	136
	xgapop 60.0 , xgapext 60.0	U	35	7	1.3	140
	Ygapop 60.0 , Ygapext 60.0	O	36	7	1.3	149
	Fgapop 6.0 , Fgapext 7.0		37	7	1.2	150
	6.0		38	7	1.2	153
		O	39	7	1.3	164
searched:	141681 seqs, 52070155 residues	O	40	7	1.3	164
7		U	41	7	1.3	164
Word Size:	ı	O	42	7	1.3	164
		O	43	7	1.3	164
Total number of	Total number of hits satisfying chosen parameters: 283186	U	44	7	1.3	165
A Transfer of the State of the	× 11	O	45	7	1.3	173

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

B ID Description	1 ING CAMBA O865w6 camelus bac	Q865×1	Q45658]	1 YVEL_BACSU P71051 bacillus si	1 YCBC_ECOLI P36565 escherichia	P31009	Q91919 1	1 PHDK_NOCSK 024723 nocardioide	09z2d3		P23389 1			1 Y018 MYCPN P75093 mycoplasma	P30182	1 YJ9H YEAST P47171 saccharomyc	08iuq5	
igth D	166	166	224	227	259	267	371	473	512	600	646	739	815	1030	1473	1648	2567	7117
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Wed Jul 14 08:56:08 2004

Alignment Scores:

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Query Match:

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  lymphocytes.
-!- SIMILARITY: Belongs to the type II (or gamma) interferon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
23937B814759328F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytokine, Antiviral, Growth regulation, Glycoprotein, Signal. SIGNAL 1 20 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERFERON GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002069; IFN-gamma.
Pfam; PF00714; IFN-gamma; 1.
ProDom; PD002435; IFN-gamma; 1.
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39 39 N-
106 106 N-
166 AA; 19475 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB107652; BAC75389.1; -.
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CARBOHYD
SEQUENCE
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-:- COFACTOR: Two heme groups which are not covalently bound to the protein (By similarity).
-:- SUBUNIT: THE MAIN SUBUNITS OF THE MENAQUINONE:CYTOCHROWE C COMPLEX ARE: CYTOCHROME B, THE RIESKE PROTEIN AND A 22/29 KDa CYTOCHROME B/C SUBUNIT. -i-SUBCELLUTAR LOCATION: Integral membrane protein (Potential). -i-SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY. CORRESPONDS TO THE AMINO END OF MITOCHONDRIAL CYTOCHROME B. MEDLINE=96218169; PubMed=8647852; Sone N., Tauchiya N., Inoue M., Noguchi S.; Hacillus stearothermophilus qur operon encoding Rieske FeS protein, cytochrome b6, and a novel-type cytochrome c1 of quinol-cytochrome c reductase.", J. Biol. Chem. 271:12457-12462(1996). Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus. Menaquinol-cytochrome c reductase cytochrome B subunit Conservative: Mismatches: 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 224 AA Length: Matches: Indels: US-09-270-437D-5 (1-1708) x ING_LAMGL (1-166) EMBL, D83789; BAA12117.1; -.
InterPro; IRRO0579; Cytb b6 N.
Pfam, PF00033; cytochrome b N; 1.
PROSITE; PS00192; CYTOCHROME B HENB; 1.
Electron transport; Heme; Transmembrane. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL 298 GATGTTGCGGATGGTGGCCCCCTC 275 51 PRT; 25411 MW; 36.5 8.00 100.00% 1.00.00% STANDARD; 116 146 215 94 108 224 AA; Percent Similarity: Best Local Similarity: Query Match: SEQUENCE FROM N.A. 108 196 STRAIN=K1041 BACTC TRANSMEM TRANSMEM TRANSMEM TRANSMEM METAL SEQUENCE QCRB_BACT QCRB_BACTC METAL METAL METAL Pred. No.: "Cloning and sequence analysis of cytokine cDNAs of llama and camel.", Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Produced by lymphocytes activated by specific antigens.
-cr mitogens. IFN-gamma, in addition to having antiviral activity, has important immunoregulatory functions. It is a potent activator of macrophages, it has antiproliferative effects on transformed cells and it can potentiate the antiviral and antitumor effects of the type I interferons (By similarity).
-! SUBLNIT: Honodimer. (By similarity). Lama glama (Llama). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama. Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C., Onuma M.; Cytokine; Antiviral; Growth regulation; Glycoprotein; Signal.
SIGNAL 1 20 BY SIMILARITY.
CHAIN 21 166 INTERFERSON GANMA. 39 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 166 AA; 19402 MW; 4547BC4FFC693655 CRC64; 166 0000 0000 Length:
Matches:
Conservative:
Mismatches:
Indels: 15-WAR-2004 (Rel. 43, Created) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) Interferon gamma precursor (IFN-gamma). PRT; 166 AA US-09-270-437D-5 (1-1708) x ING_CAMBA (1-166) 298 GATGTTGCGGATGGTGGCCCCTC 275 AspvalAlaAspGlyGlyProLeu 51 21 166 IN 39 39 N-1 106 106 N-1 166 AA; 19402 MW; ProDom; PD002435; IFN-gamma; 1. 36.5 8.00 100.00% 1.448 STANDARD; SEQUENCE FROM N.A. Percent Similarity: Best Local Similarity: NCBI_TaxID=9844;

Alignment Scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97124193; PubMed=8969506;
Fabret C., Quentin Y., Chapal N., Guiseppi A., Haiech J., Denizot F.,
"Integrated mapping and sequencing of a 115 kb DNA fragment from
Bacillus subtilis: sequence analysis of a 21 kb segment containing
the sigt locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Denizot F.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423,
                                                                                                                                                                                                                                                                                                                                                                                         YVEL BACSU STANDARD; PRT; 227 AA. P71051; 008170; 28-F2B-2003 (Rel. 41, Created) 28-F2B-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Putative tyrosine-protein kinase yveL (EC 2.7.1.112).
  0 80000
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  Length:
Matches:
Conservative:
Mismatches:
                                                                                                      Indels:
Gaps:
                                                                                                                                                                                    US-09-270-437D-5 (1-1708) x QCRB_BACTC (1-224)
                                                                                                                                                                                                                                      786 CTCCCAGCAGCGTTACTGGGGCTG 809
                                                                                                                                                                                                                                                                       200 LeuProAlaAlaLeuLeuGlyLeu 207
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SEQUENCE FROM N.A.
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                                               Percent Similarity:
Best Local Similarity:
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                                                                                                      Query Match:
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ID YCBC_ECOLI

STANDARD; PRT; 259 AA.

AC P36365; P75846;

DT 01-UDN-1994 (Rel. 29, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 36, Last annotation update)

GN YCBC OR 21267 OR ECS1003.

GN Escherichia coli, and

GN Escherichia; Briterobacteriales;

GN NCBI TaxID=562, 83334;

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OShima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
OShima T., Alba H., Baba T., Fujita K., Kanai K., Kashimoto K.,
Kiemura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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STRAIN=K12 / MG1655;
MEDLINE=9426617, PubMed=9278503;
Blattener F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Mau B., Shao Y.,
Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                     CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A70036; A70036.
Dubilist; BG11860; yvel.
InterPro; IPR005702; EPES synthesis.
TIGRRAMs; TIGRO1007; eps.fam; 1.
Hypothetical protein; Transferase; Tyrosine-protein kinase;
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Matches:
Conservative:
Mismatches:
Indels:
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Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 227 AA;
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RESULT 6
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIR-6157:147 / RIMD 0509952;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Irahii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12:";
                                       SEQUENCE FROM N.A.

STRAIN-O157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074933; PubMed=11206551;

MEDLINE-21074933; PubMed=11206551;

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Grosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., "Genome sequence of enterchaemcerhagic Escherichia coli 0157:H7.";

Nature 409:529-533(2001).
corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94232180; PubMed=7513784;
Feng J., Yamanaka K., Niki H., Ogura T., Hiraga S.;
"New Kiling system controlled by two genes located immediately
upstream of the mukB gene in Escherichia coli.";
Mol. Gen. Genet. 243:136-147(1994).
                                                                                                                                                                                                                                                                                                                                                                                          [5]
SEQUENCE OF 1-170 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12 / W3110;
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Cramton S.E., Laski F.A.; "String of pearls encodes Drosophila ribosomal protein S2, has Minute-like characteristics, and is required during oogenesis."; Generics 137:1039-1088(1994).

SEQUENCE FROM N.A.

SEQUENCE FROM N.A. MEDLINE=95073591; PubMed=7982558;

Drosophila melanogaster (Fruit fly).
Brusaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

RS2_DROME STANDARD; PRT; 267 AA. P31009; Q9VL74; STANDARD; Created) 01-JTL-1993 (Rel. 31, Last sequence update) 10-OCT-2003 (Rel. 31, Last sequence update) 40S ribosomal protein S2 (Strings of pearls protein).

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REALINE-SOURDANCE FROM N.A.

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-!-SIMILARITY: Belongs to the SSP family of ribosomal proteins.
-!-SIMILARITY: Contains 1 SS DRBM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Canton-S;
BUDINE-3181212; PubMed-8441641;
Barrio R., del Arco A., Cabrera H.L., Arribas C.;
"Cloning and analysis of the S2 ribosomal protein cDNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000).
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259 0 0 0 0

Matches: Conservative: Mismatches: Indels:

34.5 8.00 100.00% 100.00% 1.448

Percent Similarity: Best Local Similarity:

Score:

Query Match:

Alignment Scores:

US-09-270-437D-5 (1-1708) x YCBC_ECOLI (1-259)

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RESULT
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            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=20294882; PubMed=10833454;
MATSHMOTO M., Salto T., Takasaki J., Kamohara M., Sugimoto T.,
Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuichi K.;
"An evolutionarily conserved G-protein coupled receptor family, SREB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed in the central nervous system.";
Biochem. Biophys. Res. Commun. 272:576-582(2000).
-!- FUNCTION: Orphan receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S5 DRBM.

GG -> PP (IN REF. 3).

K -> R (IN REF. 3).

ADA22CD28F100743 CRC64;
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Matches:
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 Selved receptor expressed in brain 2
SREB2.
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20
194
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ID GP85_BRARE
AC Q91919;
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DB:
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iwabuchi T., Harayama S.;
"Biochemical and genetic characterization of 2-carboxybenzaldehyde dehydrogenase, an enzyme involved in phenanthrene degradation by Nocatorides sp. strain KP7.";
U. Bacteriol. 179:6488-6494(1997).
-!- FUNCTION: PROBABLY INVOLVED IN THE TRANSPORT OF 1-HYDROXY-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.

N-LINKED (GLCNAC. . ) (POTENTIAL)

N-LINKED (GLCNAC. . ) (POTENTIAL)

N-LINKED (GLCNAC. . ) (POTENTIAL)
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Nocardioides sp. (strain RP7).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Propionibacterineae, Nocardioidaceae, Nocardioides.
NCBI_TaxID=35761;
                                                        ZFIN; ZDB-GENE-000710-2; sreb2.
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; FALSE_NEG.
PROSITE; PS0262; GPROTEIN RECEP_F1_1; FALSE_NEG.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family.
                                                                                                                                                                                                                                                                                             3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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F6F6175ED3A348C2 CRC64;
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CYTOPLASMIC (POTENTIAL).
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15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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41954 1
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                                                                                                                                                                                                                     AA;
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288
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                      919
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                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                               No.:
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
Y018 MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                     Y018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;

    -!- SIMILARITY: Belongs to the sugar transporter family.

                                                                                                                                                                                                1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
8 (POTENTIAL).
                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                           9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                             EMBL, AB000735, BAA23264.1; -
InterPro; IPR00714; MFS.
InterPro; IPR005829; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
Pfam, PR00813; Sugat Tri, 1.
PROSTIE; PS50850; MFS; 1.
PROSTIE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSTIE; PS00217; SUGAR_TRANSPORT_1; 7ALSE_NEG.
Transport; Transmembrane; Inner membrane.
DOMAIN.

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                       3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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D6D765D376260D8A CRC64;
                                                                                                                                                                                                                     2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nonsyndromic hearing impairment protein 5 homolog.
DFNAS OR DFNASH.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 GlnGlySerGlyLeuLeuValLeu 284
                                                                                                                                                                                                                                                                                                                                                                                                                                        49109 MW;
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Best Local Similarity:
Query Match:
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Pred. No.:
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ID DFNS_MOUSE
AC Q9Z2D3;
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TRANSMEM
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TRANSMEM
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SEQUENCE
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                                                          Van Laer L., Huizing E.H., Verstreken M., van Zuijlen D., Wauters J.G., Bossuyt P.J., Van de Heyning P., Mcduirt W.T., Smith R.J.H., Willems P.J., Legan P.K., Richardson G.P., Van Camp G., "Nonsyndromic hearing impairment is associated with a mutation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATC 33530 / G-37;
MEDLINE=5602346; PubMed=7569993;
MEDLINE=5602346; PubMed=7569993;
MEDLINE=5602346; PubMed=7569993;
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fleischmann R.D., Maidman J.F., Small K.V., Sandusky W., Fuhmann J.L., Wolygen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma genitalium.
Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13AFB8627773C4A5 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                Nat. Genet. 20:194-197(1998).
-!- SIMILARITY: BELONGS TO THE DFNS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-270-437D-5 (1-1708) x DFN5_MOUSE (1-512)
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TISSUE=Cochlea;
MEDLINE=98442658; PubMed=9771715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF073309; AAC69325.1; -.
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SEQUENCE 512 AA; 56630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1889850; Dfnash.
InterPro; IPR007677; DFNAS.
InterPro; IPR007681; Mobl.
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MOD_RES
MOD_RES
CONFLICT
CONFLICT
  "Primary
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                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
WCBI_TaxID=9913,
                                                                                                                            C.A. III;
by using random
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
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                                               SEQUENCE OF 209-309 AND 371-471 FROM N.A. STRAIN=ATCC 33530 / G-37; MEDLINE-84075230; PubMed=8253680; Hutchison (Pectron S.N., Hu P.-C., Bott K.F., Hutchison "A survey of the Mycoplasma genitalium genome ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGI_BOVIN
P23369, 002707;
PC-3369, 002707;
PC-2001 (Rel. 20, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annocation update)
PECTECOGRAPHIN I precursor (SGI) (Chromogramin peptide, Secretolytin).
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1172 AATTTGACGGCAGCTGAGGTGGTA 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515 AsnLeuThrAlaAlaGluValVal
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MEDLINE-91223091; PubMed-2025642;
Bauer J.W., Fischer-Colbrie R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
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8.00
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Query Match:
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SG3_B

DT SG3_B

DT 01-NO

DT 16-NO

DT 28-PE

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OC BUKAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION OF SECRETOLYTIN.

MEDLINE=96184581; PubMed=8603705;
Strub J.M., Hubert P., Nullans G., Aunis D., Metz-Boutigue M.-H.;
Strub J.M., Fubert P., Nullans G., Aunis D., Metz-Boutigue M.-H.;
peptide (614-626), is correlated with peptide structure.";
FEBS Lett. 379-278-278(1996).
-I-FUNCTION: Secretogranin I is a neuroendocrine secretory granule protein, which may be the precursor for other biologically active peptides. The 16 pairs of basic AA distributed throughout its sequence may be used as proteolytic cleavage sites.
-I-FUNCTION: Secretolytin has antibacterial activity.
-I-SUBCELBULAR LOCATION: Neuroendocrine and endocrine secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Addenal chromaffin;
MEDLINE=5526269; PubMed=7744058;
Strub J.-M., Garcia-Sablone P., Lonning K., Taupenot L., Hubert P.,
Strub J.-M., Aunis D., Metz-Boutigue M.-H.;
"Processing of chromogranin B in bovine adrenal medulla.
Identification of secretolythi, the endogenous C-terminal fragment of
residues 614-626 with antibacterial activity.";
Eur. J. Biochem. 229:356-368(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: O-glycosylated (Probable). SIMILARITY: Belongs to the chromogranin / secretogranin protein
                                                                                                                                                                                                                                                     ğ
                                                                                                                                                                                                             Yoo S.H., Kang Y.K., "Identification of the secretory vesicle membrane binding region
                                                                                                                                                                                                                                                                                                                                                                                                                                  Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto E.J., Thomas G., Civelli O., Viveros O.H.; Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
structure of bovine chromogranin B deduced from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAWK PEPTIDE.
SECRETOLYTIN.
BY SIMILARITY.
SULFATION (POTENTIAL).
SULFATION (BY SIMILARITY).
N -> S (IN REF. 1).
N -> D (IN REF. 2).
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PRIMES, PR06559, CHROMOGRANIN.
PROSITE; PS00422; GRANINS 1; 1.
PROSITE; PS00423; GRANINS 2; 1.
SULfation; Cleavage on paīr of basic residues; Signal.
SIGNAL 1 20
GRAIN 21 646
SECPETALORINE 1 646
                                                               Biochim. Biophys. Acta 1089:124-126(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X55027, CAA38846.1; -.
EMBL, U88551, AAC48720.1; -.
EMBL, X55489, CAA39109.1; -.
PIR, 515901, 515901.
InterPro, IPR001819, Chromogranin_AB.
InterPro, IPR001990; Granin.
                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Adrenal medulla;
MEDLINE-97282588; PubMed-9136897;
                                                                                                                                                                                                                                                                                chromogranin B.";
FEBS Lett. 406:259-262(1997).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-646 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Adrenal medulla;
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us-09-270-437d-5.rsp

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CYTRAIN-BMRI; TISSUB-Amamary gland;
WEDLINE-22388257; PubMed-12477932;
WEDLINE-22388257; PubMed-12477932;
MEDLINE-22388257; MEDLINE-234, MEDLINE-234;
MEDLINE-234, MEDLINE-234;

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Proc. Natl. Acad. Sci. U.S.1. 99:16899-16903 (2002).

-!- FUNCTION: Transcriptional regulator that acts as repressor or activator. Binds, in-vitro, to NF-E2 binding sites. Rlay important roles in coordinating transcription activation and repression by MAFK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c;
MEDLINE=97042438;
MEDLINE=97042438;
MEDLINE=97042438;
SURVEDENTY STRAIN STREET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Transcription regulator protein BACH1 (BTB and CNC homolog 1).
      (IN REF. 3).
                              T -> M (IN REF. 2).
H -> R (IN REF. 2).
F -> R (IN REF. 2).
H -> L (IN REF. 3).
M -> V (IN REF. 3).
420DB1178FD9E415 CRC64;
                                                                                                                                                                                                                                                                                            64
8 0 0 0 0
0 0 0
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Matches:
Conservative:
Mismatches:
          FRSPRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-270-437D-5 (1-1708) x SG1_BOVIN (1-646)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         789 CCAGCAGCGTTACTGGGGCTGCTC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ProAlaAlaLeuLeuGlyLeuLeu 10
      SEAPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                Σ
                                                                                                                                                                                                                                                                                            30.8
8.00
100.00%
100.00%
1.43%
98
181
261
386
481
597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
93
181
261
386
481
597
646 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
CONFLICT
CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
BAC1 MOU
P97302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                               Score:
SPETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005634; C:nucleus; IDA.

R GO; GO:0005515; F:protein binding; IPI.

R GO; GO:0005515; F:protein binding; IPI.

R GO; GO:0006355; F:ranscription factor activity; IDA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.

R InterPro; IPR00101; BUE POZ.

R InterPro; IPR00112; Leuzip Jun.

R InterPro; IPR00482; TE DZIP.

R Pfam; PF00170; bZIP; 1.

R Pfam; PF00170; bZIP; 1.

R PRINKS; PR00043; LEUZIPRUUN.

R PRINKS; PR000318; BELZ; 1.

SWART; SW00318; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSS0097; BTB; 1.
PROSITE; PSS0217; BTSP; 1.
PROSITE; PS00065; BZIP BASIC; 1.
Transcription regulation; Activator; Repressor; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bácteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
                           -!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Belongs to the bZIP family. CNC subfamily.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BTB.
BASIC MOTIF.
LEUCINE-ZIPPER.
CE2DE606B05F6E32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA gyrase subunit B (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                815 AA.
   SUBUNIT: Heterodimer of BACH1 and MAFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     987 ATACGAACTTTGGAGTCAGGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 IleArgThrLeuGluSerGlyVal
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STRAIN-ER-15;
MEDLINE-98304088; PubMed=9639935;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D86603; BAA13137.1; -.
EMBL; BC057894; AAH57894.1; -.
HSSP; P34707; ISKN.
TRANSFAC; T04793; -.
MGD; MGI:894680; Bach1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 BT
580 BA
610 LE
81373 MW;
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588 67
739 AA)
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Best Local Similarity:
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033367;
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Query Match:
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SO THE TAKE BEAUTH OF THE SOLUTION OF THE SOLU
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xie S., Lam E.
                                   pneumoniae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
TOP2 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
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Paitan Y., Boulton N., Ron E.Z., Rosenberg E., Orr E.;
"Molecular analysis of the DNA gyrB gene from Myxococcus xanthus.";
Microbiology 144:1647(1998).

-!- FUNCTION: DNA gyrase negatively supercoils closed circular double-stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings.
-!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
-!- GAUBUNIT: Made up of two chains. The A chain is responsible for DNA breakage and rejoining, the B chain catalyzes ATP hydrolysis. The enzyme forms an AZB2 tetramer.
-!- SIMILARITY: Belongs to the type II topoisomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical halicase MG018/MG017/MG016 homolog (D12_orf1030).
MPN020 OR MP134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В.-С.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRPAMS; TIGR01059; GYTB; 1.
PROSITE; PS00177; TOPOISOMERASE II; 1.
TOPOISOMERASE; ISOMERASE; ISOMERASE; SEQUENCE 815 AA; 89636 MW; 3867685FBB805B32 CRC64;
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STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; Pubmed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR000258; DNA_gyraseB_C.
InterPro; IPR0001241; DNA_topoisoII.
InterPro; IPR001241; DNA_topoisoII.
InterPro; IPR006171; Toprim dom.
Pfam; PF00204; DNA_gyraseB_C; I.
Pfam; PF003018; NA_gyraseB_C; I.
Pfam; PF07518; ATPase C; I.
Pfam; PF07518; Toprim; I.
PRINTS; PR00418; TP12PAMILY.
ProDom; PD14963; DNA_gyraseB_C; I.
SMART; SM00433; TOP2C; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGGTGGATCACACCTCAGTGGG 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 GluGlyGlySerHisLeuSerGly 296
                                                                                                                                                                                                                                                                                                                       EMBL; AJ000543; CAA04176.1; -. HSSP; P06982; 1AJ6.
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8.00
100.00%
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1.43%
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Best Local Similari
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P75093;
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'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPEZ ARATH STANDARD; PRT; 1473 AA.
P3018; 038807;
01-APR-1993 (Rel. 25, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA topoisomerase II (EC 5.99.1.3).
Arabidopsis thaliana (Mouse-ear creat)
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollaophyta; Embryophyta; core eudicots; rosids;
eurosids II. Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of a DNA Topoisomerase II cDNA from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Helicase, ATP-binding; Complete proteome. NP BIND 603 610 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xie S., Lam E.; "Abundance of nuclear DNA topoisomerase II is correlated with
                                  Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
-!- SIMILARITY: TO M.GENITALIUM MG016, MG017 AND MG018.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-cv. Columbia, and cv. Kas-1; MEDLINE=95140639; PubMed=7838729;
                                                                                                                                                                                                                                                                                                     PIR; $73460; $73460.

InterPro; IPR001410; DEAD.

InterPro; IPR001650; Helicase C.

InterPro; IPR000330; SNF2 N.

InterPro; IPR000330; SNF2 N.

InterPro; IPR00271; InterPro; IPR00757; InterPro; IPR00757; Nelicase C.

Pfam; PF00176; SNF2 N; I.

Pfam; PF00176; SNF2 N; I.

SWART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Physiol, 106:1701-1702(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
MEDLINE=95148754; PubMed=7846176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119601 MW;
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100.00%
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The profileration in Arabidopsis thaliana, ', R. Wicletc Acids Res. 22:5729-5736(1994).

R. WICLETC Acids Res. 22:5729-5736(1994).

R. WICLETC Acids Res. 22:5729-5736(1994).

R. SEQUENCE FROW N.A.

R. STRINGENCY. Columbia.

R. MIDINER-CO. Columbia.

R.
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Length:
Matches:
Conservative:
Mismatches:
Indels:

27.7 8.00 100.00% 100.00% 1.44%

> Percent Similarity: Best Local Similarity: Query Match:

Pred. No.:

US-09-270-437D-5 (1-1708) x TOP2_ARATH (1-1473)

Search completed: July 13, 2004, 12:31:31 Job time : 31.5 secs

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Sequence 2, Appli
Sequence 348, App
Sequence 348, App
Sequence 446, App
Sequence 448, App
Sequence 449, App
Sequence 449, App
Sequence 427, App
Sequence 427, App
Sequence 427, App
Sequence 427, App
Sequence 176, App
Sequence 116, App
Sequence 1116, App
Sequence 1114, App
Sequence 1117, App
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 500, Application US/10313986
; Edquence 500, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: McMabb, Andria
APPLICANT: Read Steven G.
APPLICANT: Read Steven G.
APPLICANT: Read Steven G.
APPLICANT: Read Steven G.
APPLICANT: Nang, Tongcong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C19
CURRENY APPLICATION NUMBER: US/10/313,986
CURRENY FILING DAIE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
; SOFTWARE FRAESQ for Windows Version 4.0
              ALIGNMENTS
 Homo sapiens
 10-313-986-500
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rived by analysis of the total score distribution.
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| cgg12_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

    protein search, using frame_plus_n2p model

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US-09-735-705-348
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US-U9-735-748
US-U9-735-748
US-U0-725-748
Sequence 348, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Fan, Liqun
APPLICANT: Ranger, Ghaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Ranger, Gary R.
APPLICANT: Ranger, Gary R.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Ailun
APPLICANT: Wang, Ailun
APPLICANT: Skelky Yasair A.W.
APPLICANT: Wang, Ailun
APPLICANT: Ranger, Nebert A.
APPLICANT: Ranger, Neb.11
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
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Matches:
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Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
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CURRENT APPLICATION NUMBER: US/09/850,716A, CURRENT FILING DATE: 2001-05-07
CURRENT FILING DATE: 2001-05-07
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
TYPE: PRT
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| ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
                                                                                         CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCCCGAAACA 967
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Sequence 348, Application US/09897778

Patent No. US20020147143A1

SGENERAL INPORMATION:
APPLICANT: Warng Tongtong
APPLICANT: Farnger, Gary R.
APPLICANT: Farnger, Gary R.
APPLICANT: Farnger, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedranabe, Yoshihiro
APPLICANT: Wedranabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121455C16
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ 1D NOS: 467

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 348
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Indels:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Db 467 GlnGlyArgIleTyrGlyLysIleLysGluGluAsnPheValSerProLysGluGluVal 486 Qy 1088 AAGCTGGAGACCCACATACGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT 1147 Db 487	AAGAGAC 		Oy 1268 CAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAG 1324	Oy 1325 AAGGACAGAGTAACCAGGCACAGGAAGAAG 1360 Db 567 LysalaLeuGlnSerGlyProProGlnSerArgArgLys 579	RESULT 6 US-09-897-778-446 Sequence 446, Application US/09897778 Patent No. US2002014714341		; APPLICANT: Vedvick, Thomas S. ; APPLICANT: Vedvick, Thomas S. ; APPLICANT: Vedvick, Voshihiro ; APPLICANT: Handacon Dohert A.	APPLICANT: Peckham, David N.; APPLICANT: Fanger, Neil ; ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ; TITLE OF INVENTION: AND DISCOVERY OF THAT OF ANTONION.	FILE REFERENCE: 210121.455C16 CURRENT APPLICATION NUMBER: US/09/897,778 CURRENT FILING DATE: 2001-06-28 NUMBER OF SEO ID NOS: 467	SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 446 LENGTH: 579 TYPE: PRT	; ORGANISM: Homo sapiens US-09-897-778-446	Pred. No.: 1.26e-121 Length: 579 Score: 1639.00 Matches: 336 Percent Similarity: 93.89\$ Conservative: 44 Best Local Similarity: 74.17\$ Mismaches: 57	52.70% Indels: 9 Gaps: 708) x 115-09-897-778-446 (1-579)	Oy 32 CGGGAGCCATCATGAATGGCCACCAGTTGGAGAACCATGCCTGAAGGTCTCC 91	TACATCCCCGATGAGCAGATAGCAAGGGACCTGAGAATGGGCGCCGAGGG 14	143 GCTTTGGCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGGGGGGCCCCAGCC 20 173 GLTTGGCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGGGGGGCCCCAGCC 20 173 GlvLeuGlvGlnArdGlvSerSerArGlnGlvGlvSerPro	203 AAGCAGCAGTAGACCCCCTTCGGCCCCCCCAGTATGTGGCTCCCCAGTATGTGGGTGCCCCCAGTATGTGGGTGCCCAGTATGTGGGTGCCCAGTATGTGGGTGCCCAGTATGTGGGTGCCCAGTATGTGGGTGCCCAGTATGTGGGTGCCCAGTATGTGGGTGCCCAGTATGTGGGTGCCCAGTATGTGTGTG

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GGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTAGTAGTACCAAGAGAC 1207
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|ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
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              AAGGGGCCCATCGAGAATTGTTGCAGGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAG
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US-10-007-700-348
Sequence 348, Application US/10007700
Sequence 348, Application US/10007700
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Li, Samual X.
APPLICANT: Handerson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNOWILL, Patricia D.
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| ProGluGlyThrSerAlaAlaCysLysSer1|eLeuGluIleMetHisLysGluAlaGln
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Sequence 449, Application US/09897778

Sequence 449, Application US/09897778

Sequence 449, Application US/09897778

Sequence 449, Application US/09897778

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APPLICANT: Warnerakis, Margarita

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Percham, Daridk

APPLICANT: Henderson, Robert A.

APPLICANT: Peckham, David W.

APPLICANT: Percham, David W.

APPLICANT: Panger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121-455C16

CURRENT APPLICANTEN AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121-455C16

CURRENT APPLICANTEN AND DIAGNOSIS OF LUNG CANCER

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4499
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Matches:
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Publication No. US20030064947A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasır A.W.
APPLICANT: Li, Samual X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Pecken, Darrick
APPLICANT: Pecken, Darrick
APPLICANT: Pecken, Darrick
APPLICANT: Pecken, David W.
APPLICANT: Pecken, David W.
APPLICANT: Pecken, Paris
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APPLICANT: Fanger, Nail
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Peckman, David W.
APPLICANT: Cai, Feng
APPLICANT: Cai, Feng
APPLICANT: Coly Compositions AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 348
LENGTH: 579
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Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Homo
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390 ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENT 210121.455C17.700
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastsEQ for Windows Version 4.0
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; Publication No. US20030064947A1
; GENERAL INFORMATION:
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APPLICANT: Wang, Aljun
APPLICANT: Edicking, Asir A.W.
APPLICANT: Li, Samual X.
APPLICANT: Li, Samual X.
APPLICANT: Mandel D.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Neil
APPLICANT: Fanger, Neil
APPLICANT: Panger, Neil
APPLICANT: Panger, Neil
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Garter, Darrick
APPLICANT: Watcanabe, Yoshihiro
APPLICANT: Garter, Darrick
APPLICANT: Gerter, Darrick
APPLICANT: Gerter, Darrick
APPLICANT: Gerter, Darrick
APPLICANT: Gerter, Darrick
APPLICANT: Peckman, David W.
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LysGlnLysProCysAspLeuProLeuArgLeuLeuValProThrGlnPheValGlyAla 209
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                      THE THERAPY
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Conservative:
Mismatches:
Indels:
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                    CANCER
APPLICANT: Foy, Teresa M.
TITE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCE; FILE REFERENCE: 210121.455C17
CURRENT ETHING DATE: 201-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 579
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; ORGANISM: Homo sapiens
US-10-007-700-446
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apiens 1.26e-121 Length: 5	ative: 44 hes: 57 16	US-09-270-437D-5 (1-1708) x US-10-007-700-449 (1-579) QY	92 TACATCCCCGAGGAGATAGCA	Qy 203 AAGCAGCAAGAAAGTGGACATCCCCTTCGGCTCCTGGTGCCCAGTATGTGGGTGCC 262	Oy 263 ATTATIGGCAAGGGGCCACCATCGGAACATCACAAAACAGACCCAGTCCAAGATA 322	Oy 323 GACGTGCATAGGAAGGAGAACGCAGGTGCAGAAAAGCCATCAGTGTGCACTCCACC 382 	Oy 383 CCTGAGGGCTGCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAG 442	OY 443 GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGG 502	Oy 503 CGICTCATTGGCAAGGAAGGAACCTGAAGAAGGTAGGAAGAAACGAGAAAA 562 	Oy 563 ATCACCATCTCCTGTTGCAAGACCTTAACCCTTTACAACCCTGAGAGCACCATCACTGTG 622	Oy 623 AAGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAATAATGAAGAAGTTCGGGAG 682 	Oy 683 GCCTANGAGAATGAGGCTGCCANGAGCTCTCACCTGATCCCTGGCCTGAC 736 :::	Oy 737 CTGGCTGCTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCT 787	Oy 788 CCCAGCAGCGTTACTGGGGCTGCTCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGG 847	OY 848 ATGGTGCAGGTGTTTATCCCGCCCAGGCAGTGGGGCGCCATCATCGGCAAGAAGGGGAG 907

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Sequence 446, Application US/10117982

Publication No. US20030138438A1

GENERAL INFORMATION:
APPLICANT: Forger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Mericle, Barbara
APPLICANT: Spies, Gregory A.
APPLICANT: Spies, Gregory A.
APPLICANT: Spies, Gregory A.
APPLICANT: Spies, Gregory A.
APPLICANT: Fan, Liqun
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: 484
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 484
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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Best Local Similarity:
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GGGACAGAGTRACCAGGCCCAGGCACC SALaLeuGlnSerGlyProProGlnSerAr Application US/10117982 Application US/10117982 ATON: Y, Teresa M. ATON: ATON	US-09-270-437D-5 (1-1708) x US-10-117-982-449 (1-579) Qy 32 CGGCGAGCCATCATGAAGCTCAATGGAGAACCATGCCCTGAAGGTCTC 91 133 ArgGlaAlaLeuAspLysLeuAsnGlyPheGlaLeuGluAsnPheThrLeuLysValala 152 Qy 92 TACATCCCCGATGACAGAATGGCAC-CAGGACCTGAGAATGGCCGCGAGGGC
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APPLICANT: Kalos, Michael D.
APPLICANT: Mericle, Barbara
APPLICANT: Gregory A.
APPLICANT: Fan, Liqun.
APPLICANT: Fan, Liqun.
APPLICANT: Wang, Tongrong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C18
CURRENT APPLICATION NUMBER: US/10/117,982
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 484
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 579
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ORGANISM: Homo sapiens
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SerTyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsn 369
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     AspileLysPheThrGluGluIleProLeuLysIleLeuAlaHisAsnAsnPheValGly
                                                                  ATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGGACCATCACTGTG
                                                                                                                                                GCCTATGAGAATGATGTGGCTGCCATGAGC-----TCTCACCTGATCCCTGGCCTGAAC
                                                                                                                                                                                        CTGGCTGCTGTAGGTCTTTTCCCAGCTTCAGCGCAGTCCCGCCG------CCT
                                      CGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAA
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| LysAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
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US-10-117-982-480
IS-10-117-982-480
Septication US/10117982
Publication No. US20030138438A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Foy, Teresa M.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
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Percent Similarity: 83.89% Conservative: 44 Best Local Similarity: 74.17% Mismatches: 57 Query Match: 52.70% Indels: 16 DB: 15 Gaps: 9 US-09-270-437D-5 (1-1708) x US-10-313-986-348 (1-579)	Qy 32 CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCC 91	CCGATGAGCAGATAGCACAGGGACCTGAGAATGC 	Qy 143 GGCTTTGGCTCTCGGGGTCAGCCCCGCCAGCCTGTGGCAGGGGGGCCCCAGCC 202	Qy 203 AAGCAGCAGGAAGGAACATCCCCCTTCGGCTGCCCACCCA	Qy 263 ATTATTGGCAAGGAGGCCACCATCCGCAACATCACAAAACAGACCCCAGTCCAAGATA 322	Qy 323 GACGTGCATAGGAAGGAGAACGCAGGAGCTGAAAAAGCCATCAGGTGTGCACTCCACC 382	Qy 383 CCTGAGGCTGCTCCTCCGCTTGTAAGATGATTATGCATAAGAGGCTAAG 442	QY 443 GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGG 502	Qy 503 CGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGCAAGATACCGAGACAAAA 562	Qy 563 ATCACCATCTCCTCGTTGCAAGACCTTACCCTTACAACCCTGAGAGGACCATCACTGTG 622		:::	OY 737 CTGGCTGCTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGCGCAGCGCGCGC	OY 788 CCCAGCAGCATACTGGGGCTGCTCCTATAGCTCCTTATGCAGGCTCCCGAGCAGCAG 847	Qy 848 ATGGTGCAGGCCCCAGGCAGTGGCCCATCATCGGCAAAGAGGGCAG 907	Qy 908 CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACA 967	968 CCTGACTCCAAAGTTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCT 10
Db 350 SerTyrGludsnAspileAlaSerMetAsnLeuGlnAlaHisLeulleProGlyLeuAsn 369 Qy 737 CTGGCTGCTGTAGGTCTTTTCCCAGCTCATCCAGCGCAGTCCCGCGGCCT 787 Db 370 LeuAsnAlaLeuGlyLeuPheProProThrSerGlyMetProProProThrSerGlyPro 389	Oy 788 CCCAGCAGCGTTACTGGGGCTGCTCCTTTATGCAGCTCCCGAGCAGGAG 847	OY 848 ATGGTGCAGGTGTTTATCCCGCCCAGGCAGTGGGCGCCATCATCAGCAAGAAGGGCAG 907	Qy 908 CACATCAAACAGCTCTCCCGGTTTGCCACCACCATCAACATTGCACCACCGGAACA 967	Qy 968 CCTGACTCCAAAGTTCGTATGGTDATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCT 1027	Qy 1028 CAGGGAAGAATCTATGGCAAACTCCAAGGAGAAACTTCTTTGGTCCCAAGGAGGAGGAGTG 1087	Oy 1088 AAGCTGGAGACCACATACGTGTCCCAGCATCACCAGCTGGCCGGGTCATTGGCAAAGGT 1147	Qy 1148 GGAAAAACGGIGAACGAGTTGCAGAATTTGACGCCAGCTGAGGTGGTAGTACCAAGAGAC 1207	Qy 1208 CAGACCCCTGATCAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGT 1267	Qy 1268 CAGATGGCTCAACGGAAGATCCGGGACATCCTGGCCCCAGGTTAAGCAGCAGCATCAG 1324	Qy 1325 AAGGACACAGTAACCAGGCCCAGGAGGAAG 1360	RESULT 15 US-10-313-986-348 ; Sequence 348, Application US/10313986 ; Publication No. US20030236209A1 ; GENERAL INFORMATION:	; APPLICANT: Foy, Teresa M. ; APPLICANT: McNabb, Andria ; APPLICANT: Watanabe, Yoshihiro	; APPLICANT: Reed, Steven G. ; APPLICANT: Wang, Tongtong ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY : TITLE OF INVENTION: AND DIAGNOSTS OF TIME CANCED.	FILE REFERENCE: 210121.455C19 ; CURRENT APPLICATION NUMBER: US/10/313,986 ; CURRENT FILING DATE: 2002-12-04 ; NIMMED OF OF THE NOW COMMENT OF THE NEW COMMENT OF THE	SOFTWARE: PastSEQ for Windows Version 4.0 ; SEQ ID NO 348 ; LENGTH: 579	; ORGANISM: Homo sapiens ; US-10-313-986-348	Alignment Scores: Pred. No.: Score: 1639.00 Matches: 336

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1028 CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG 1087
                                                                                   1208 CAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGT 1267
                                                                                                                                  527 GlnThrProAspGluAsnAspGlnValValValLysIleThrGlyHisPheTyrAlaCys 546
447 ProAspAlaLysValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAla 466
                           1325 AAGGGA---CAGAGTAACCAGGCCCCAGGCACGAAG 1360
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US-09-261-855-2
Sequence 2, Application US/09261855A
Sequence 2, Application US/09261855A
Sequence 2, Application US/09261855A
September 100. 6255055
GENERAL INFORMATION:
APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296.95131
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATCHIN Ver. 2.0
SOFTWARE: PATCHIN Ver. 2.0
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US-09-261-855-2
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11. /Ggn2_6/ptodatca2/iaa/5A_COMB.pep:*
12. /Ggn2_6/ptodatca2/iaa/5B_COMB.pep:*
31. /Ggn2_6/ptodatca/2/iaa/6B_COMB.pep:*
41. /Ggn2_6/ptodatca/2/iaa/6B_COMB.pep:*
42. /Ggn2_6/ptodatca/2/iaa/PCTUS_COMB.pep:*
61. /Ggn2_6/ptodatca/2/iaa/PCTUS_COMB.pep:*
62. /Ggn2_6/ptodatca/2/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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GENERAL INFORMATION:
APPLICATIVE ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE REPRENCE: 560296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
SEQ ID NOS: 46
SOFTWARE: PATCHIN VEY: 2.0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                             US-09-261-855-20
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                                                                                                                                                                                                                                                                                  LENGIH: 48
                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                  234 LysGluAsnAlaGlyAlaAlaGluLysAlaIleSerValHisSerThrProGluGlyCys 253
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                                                                                                                                                              SerSerAlaCysLysMetileLeuGluIleMetHisLysGluAlaLysAspThrLysThr 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAATTGTTGCAGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCCTATGAGAAT 694
  AAGGAGAACGCAGCTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGGCTGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536 AAGGTAGAGCAAGATACCGAGACAAAATCACCATCTCCTCGTTGCAAGACCTTACCCTT 595
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US-09-261-855-18
Sequence 18, Application US/09261855A
Sequence 18, Application US/09261855A
Sequence 18, Northwall Control C
                                                                                                                                                                                                                   GCTGACGAGGTTCCCCTGAAGATCCTGGCCCCATAATAACTTTGTAGGGCGTCTCATTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGTTGCAAGACCTTACCCTTTACAACCCTGAGGACCATCACTGTGAAGGGGGCCATC
                                                                                                          TCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAACG
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Mismatches:
Indels:
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US-09-261-855-20
; Sequence 20, Application US/09261855A
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ORGANISM: Mus musculus
US-09-261-855-18
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Best Local Similarity:
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Pred. No.:
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DB:
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Sequence 17, Application US/09261855A
| Sequence 17, Application US/09261855A
| GENERAL INFORMATION:
| ATTILE OF INVENTION: (FUR. BP) AND ITS NUCLEIC ACID SEQUENCE
| TITLE OF INVENTION: (FUR. BP) AND ITS NUCLEIC ACID SEQUENCE
| FILE REFERENCE: 960296.95131
| CURRENT APPLICATION NUMBER: US/09/261,855A
| CURRENT FILING DATE: 1999-03-03
| NUMBER OF SEQ ID NOS: 46
| SOFTWARE: PARENTIN Ver. 2.0
| SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LeuLeuValProThrGlnTyrValGlyAlaIleIleGlyLysGluGlyAlaThrIleArg
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Matches:
Conservative:
Mismatches:
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; ORGANISM: Homo sapiens
US-09-643-597-176
                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GInLeuSerArgPheAlaSerAlaSerIleLysIleAlaProProGluThrProAspSer 40
21 AsnileThrLysGlnThrGlnSerLysIleAspValHisArgLysGluAsnAlaGlyAla 40
                                                                                                                         SQUENCE 19, Application US/09261855A

Faquence 19, Application US/09261855A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND IS NUCLEIC ACID SEQUENCE
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 19
LENGTH: 47
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US-09-643-597-176

US-09-643-597-176

Sequence 176, Application US/09643597

Patent No. 6426072

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Ralos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Mancy Aljun

APPLICANT: Mancy Aljun

APPLICANT: Wakely, Yasir A.W.

APPLICANT: McMeil, Patricia D.

TITLE OF INVENTION: Patricia D.

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 21011.455C11

CURRENT PILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 369

SEQ ID NO 176

LENGTH: 579

TYPE: PRT
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Matches:
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; ORGANISM: Mus musculus
US-09-261-855-19
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Query Match:
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Pred. No.:
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US-09-261-855-19
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APPLICANT: Wang, Tongtong
APPLICANT: Rai, Liqun
APPLICANT: Rangur, Chaitanya S.
APPLICANT: Rangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: McDert A.
APPLICANT: McMeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
CURRENT FILING AND DIAGNOSIS OF LUNG CANCER
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369-08-21
NUMBER OF SEQ ID NOS: 369-08-21
SEQ ID NO 348
SEQ ID NO 348
LENGTH: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 SerlysileAspValHisArgLysGluAsnAlaGlyAlaAlaGluLys 242
                                                                                                                                                                                                                                                                                        227 SerlysileAspValHisArgLysGluAsnAlaGlyAlaAlaGluLys 242
                                                                                                                                                                                                                                                                   314 TCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAA 361
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                                                                                                    Gaps:
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; Sequence 176, Application US/09480884A; Patent No. 6482597
; GENERAL INFORMATION:
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; Sequence 348, Application US/09643597
; Patent No. 6426072
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) ORGANISM: Homo sapiens

US-09-643-597-348
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Best Local Similarity:
Query Match:
                                        Percent Similarity:
Best Local Similarity:
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RESULT 11
US-09-606-421B-176
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 176, Application US/09542615A
| Sequence 176, Application US/09542615A
| Patent No. 6518256
| GENERAL INFORMATION:
| APPLICANT: Wang, Tongtong
| APPLICANT: Fan, Liqun
| APPLICANT: Fan, Liqun
| APPLICANT: Fangur, Chaitanya S.
| APPLICANT: Banger, Cary R.
| APPLICANT: Panger, Cary R.
| APPLICANT: Panger, Cary R.
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE REPERBUGE: 210121.455C8
| CURRENT APPLICATION NUMBER: US/09/542,615A
| CURRENT FILING DATE: 2000-04-14
| NUMBER OF SEQ ID NOS: 350
| SEQ ID NO 176
| LENGTH 579
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Ligun
APPLICANT: Fan, Ligun
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
TITLE OF INVENTION: GOMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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; ORGANISM: Homo sapiens
US-09-542-615A-176
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Sequence 176, Application US/09606421B
Patent No. 6531315
SGENERAL INPORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: AAI,0s, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Ranger, Gary R.
APPLICANT: Wang, Aljun
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: Seeiky, Yasir A.W.
APPLICANT: SOURCER: 210121.455C9
CURRENT FILE REFRENCE: 210121.455C9
CURRENT FILIANTON: OMPGEN: 2000-06-28
CURRENT FILIANTON: WHIGHOWS Version 3.0
SEQ ID NO 176
LENGTH: 579
314 TCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAA 361
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Branger, Cary R.
APPLICANT: Fanger, Cary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAB
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER,
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
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                                                                                                                                 Sequence 348, Application US/09542615A Patent No. 6518256; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-606-421B-176
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APPLICANT: ROSS, Jeffrey
APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE; FILE REFERENCE: 960296.95131
                                                                                                                                                                                                                                                                RESULT 12

US-09-66-421B-348

US-09-66-421B-348

Sequence 348, Application US/09606421B

Patent No. 6531315

GENERAL INPORMATION:

APPLICANT: Fan, Liqun

APPLICANT: Fan, Liqun

APPLICANT: Fancy, Machael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Sewell, Nancy

APPLICANT: Sexify, Yasir A.W.

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 21012.455509

CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SEQ ID NO 348

LENGTH: 579

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Query Match: 6.43$
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US-09-606-421B-348
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Sequence 24, Application US/09261855A
Sequence 24, Application US/09261855A
Sequence 24, Application US/09261855A
Sequence 24, Application US/09261855A
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 24
LENGTH: 48
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; Sequence 3, Application US/09261855A
; Sequence 3, Application US/09261855A
; Patent No. 625505;
; GENERAL INFORMATION:
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT PELING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
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                                                                                                                                                                                           Length:
Matches:
CURRENT APPLICATION NUMBER: US/09/261,855A CURRENT FILING DATE: 1999-03-03 NUMBER OF SEQ ID NOS: 46 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO. 21 LENGTH: 47 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                   338 GAGAACGCAGGTGCAGCTGAAAAA 361
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Query Match:
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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENCTH: 14
; TYPE: PT
; ORGANISM: Mus musculus
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                       Abp61968
Ada28817
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Abb74960
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ADA28438
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WPI; 1999-551506/46.
N-PSDB; AAZ10617.
Mus musculus.
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                       AlaAlaProTyrSerSerPheMetGlnAlaProGluGluGluMetValGlnValPheIle
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          GCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATC
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                  The present sequence represents a murine c-myc coding region determinant binding protein (CRD-BP). The presence or absence of a tumor can be determined by determining the levels of CRD-BP present in the suspect tissue, where the CRD-BP shields c-myc RNA from endonucleolytic attack and so prolongs its half-life. The methods are used for diagnossing presence or absence of a tumor in a human, especially breast, colon and pancreatic cancer. They are also used to inhibit cancer cell growth
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                                                                                                                       This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have eytostatic activity. The polypeptides and polymuleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polymucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgLeulleGlyLysGluGlyArgAsnLeuLysLysIleGluGlnAspThrAspThrLys
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                               polypeptide comprising an immunogenic portion of a lung is used for detecting and monitoring progression of lung
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Matches:
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                                                                                            English,
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                                                                                            259-261; 261pp;
                                                                                                                                                                                                                                                                                                                                                                   2.36e-144
1639.00
83.89%
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                                                                                                                                                                                                                                                                                       development of cancer
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                     Sequence 579 AA;
                                                                                            Page
                                               protein is us
in a patient.
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                                                                                                                                                                      SerTyrGluAsnAspileAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsn 369
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 AspileLysPheThrGluGluIleProLeuLysIleLeuAlaHisAsnAsnPheValGly
                                               ATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTG
                                                                                                           310 IleThrileSerProLeuGlnGluLeuThrLeuTyrAsnProGluArgThrileThrVal
                                                                                                                                                                                                              GCCTATGAGAATGATGTGGCTGCCATGAGC-----TCTCACCTGATCCCTGGCCTGAAC
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|ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu
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                                 CGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAA
                                                                                                                                                   AAGGGGGCCATCGAGAATTGTTGCAGGGCCGAGGAAATAATGAAGAAAGTTCGGGAG
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|VsAlaLeuGlnSerGlyProProGlnSerArgArgLys
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                                                                                                                                                                                                                                                                                                                                                                   fusion
                                                                                                                                                                                                                                                                                                                 The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. AB448959 to AB449300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGG
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                                                                                                                                                                                                                                         tumor polypeptides, useful for treating immune response.
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Fanger GR;
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MW, Marnerakis M,
oe Y, Peckham DW;
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Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                         Claim 2; Page 365-367; 374pp; English
                                                                                                                                    g A, Skeiky YAW, Li
Fanger N, Retter MW
Carter D, Watanabe
02-AUG-2000; 2000US-00630940.
21-AUG-2000; 2000US-00643597.
15-SEP-2000; 2000US-00662786.
9-SEP-2000; 2000US-00685696.
12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
                                                                                                                                                                                                                                            Polynucleotides encoding lung lung cancer or stimulating an
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N-PSDB; ABL49297.
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                                                                                                                                      Wang A,
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Percent Similarity:
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Mcneill PD,
Vedvick TS,
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Pred. No.:
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ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu
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LysGlyAsnValGluThrCysAlaLysAlaGluGluGluIleMetLysLysIleArgGlu
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                                                                                                                   lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
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N-PSDB; ABL49299.
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02-AUG-2000; 2
1-AUG-2000; 2
15-SEP-2000; 2
09-OCT-2000; 2
12-DEC-2000; 2
07-MAY-2001; 2
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Mcneill I
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        Mismatches:
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                                                                    1324
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GInValAlaGInArgLysIleGInGluIleLeuThrGInValLysGInHisGInGlnGIn
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nger GR, Vedvick TS;
                                                                CAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCCAGGTTAAGCAG----CAGCATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; lung tumour; cytostatic; gene therapy; vaccine
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Durham M, Fanger GR,
7, Cai F, Foy TM;
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Matches:
Conservative:
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Retter MW, D
Peckham DW,
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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Mcneill PD, Fanger N,
Carter D, Watanabe Y,
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Durham M, Fanger GR, Vedvick TS;
Cai F, Foy TM;
                                                                                                GGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGAGAC
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LysLeuGluhlaHisIleArgValProSerPheAlaAlaGlyArgValIleGlyLysGly
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           CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG
                                                     AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                      Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
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Peckham DW,
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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J, Watanabe Y,
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N-PSDB; ABQ92485.
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amount of polymucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used in the exemplification of the present
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Conservative:
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2.36e-144
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Best Local Similarity:
Query Match:
DB:
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ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer--GluThrGlu 406
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                          ATGGTGCAGGTGTTTATCCCCCCCAGGCAGTGGGCGCCATCATCGGCAAGAAGGGGCAG
                                                            CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCGAAACA
                                                                                                        GlnThrProAspGluAsnAspGlnValValVallysIleThrGlyHisPheTyrAlaCys
                                    ThrValHisLeuPheIleProAlaLeuSerValGlyAlaIleIleGlyLysGlnGlyGln
                                                                                                                               CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG
                                                                                                                                          GlnGlyArg11eTyrGlyLys11eLysGluGluAsnPheValSerProLysGluGluVal
                                                                                                                                                                           CAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGT
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                                                                                                                                                                 AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT
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PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick
Watanabe Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                             Human lung cancer associated protein sequence SEQ ID NO:446.
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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D, Watanabe Y,
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The present invention describes isolated human lung carcinoma polyuncleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polyuncleotide that hybridises to the oligonucleotide to a mount of polyuncleotide that hybridises to the oligonucleotide to a predecermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABPG1866 to ABPG1992 represent sequences used in the exemplification of the present
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| ProGluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLysGluAlaGln
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                                                                                      Claim 9; Page 372-374; 381pp; English
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Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
Mcneill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedv
Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                       New isolated polynucleotides and polypeptides useful preventing and/or treating cancer, particularly lung
                                                                                                                                                                                                                                                                                                                       Claim 9; Page 285-287; 296pp; English.
                                      99US-00285479.
99US-00466396.
99US-00476496.
                                                                      2000US-00480884.
2000US-00510376.
2000US-00542615.
                                                                                                     2000US-00606421.
2000US-00630940.
2000US-00643597.
                                                                                                                                               09-OCT-2000; 2000US-00685696.
12-DEC-2000; 2000US-0073705.
07-MAX-2001; 2001US-0085716.
28-JUN-2001; 2001US-00897778.
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1639.00
83.89%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 579 AA;
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                                                                     10-JAN-2000;
22-FEB-2000;
04-APR-2000;
28-JUN-2000;
21-AUG-2000;
21-AUG-2000;
15-SEP-2000;
       18-MAR-1998;
27-JUL-1998;
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02-APR-1999;
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30-DEC-1999;
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                     AAGGGGCCCATCGAGAATTGTTGCAGGCCCGAGCAGGAAATAATGAAGAAAGTTCGGGAG
                                                                                                                                      CCCAGCAGCGCTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAG
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                                                   GCCTATGAGAATGATGTGGCTGCCATGAGC-----TCTCACCTGATCCCTGGCCTGAAC
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| LysAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
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Vedvick TS;

for diagnosing, cancer.

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TyrileProAspGluThrAlaAlaGlnGlnAsnProLeuGlnGlnProArgGlyArgArg 172
                           for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polymucleotide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences; or degenerate variants of the above incleotide sequences; or degenerate variants of the above diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence of a recombinant human lung tumour associated protein.
The invention describes isolated polynucleotides and polypeptides useful
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AAGGGA---CAGAGTAACCAGGCCCCAGGCACGGAGGAAG
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                                                                                          Homo sapiens.
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Mcneill PD,
Carter D,
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    ATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATA 322
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| ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
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                                                                   CCTGAGGGCTGCTCCTCCTCGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAG
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The invention describes isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynucleotide comprises: any of the 22 fully defined nucleotide sequences in or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences; or degenerate variants of the above nucleotide sequences. The composition and methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence of a recombinant human lung tumour associated protein.
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PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick
D, Watanabe Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; lung cancer; gene therapy; vaccine; human; lung squamous cell carcinoma.
Recombinant human lung tumour protein L523S
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27-JUL-1998, 98US-00123912.
22-DEC-1999; 99US-00221107.
02-ARR-1999; 99US-0046396.
17-DEC-1999; 99US-00466396.
10-JAN-2000; 2000US-00480884.
22-FEB-2000; 2000US-00480884.
22-FEB-2000; 2000US-0064210.
22-AUG-2000; 2000US-00643671.
15-SEP-2000; 2000US-00643597.
15-SEP-2000; 2000US-00663997.
15-SEP-2000; 2000US-00663696.
15-DEC-2000; 2000US-00663696.
15-DEC-2000; 2000US-00685696.
15-DEC-2000; 2000US-008957786.
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988 CCTOACTCCAACTCCATACTCATACTCATACTCACCCCCACACTCCACACTCCAAC	(CORI-) CORI Wang T, Wan Moneill PD, Carter D, W
Score Score 13.96-144 Length Score 13.95	407 ThrValHisLeuPhelleProAlaLeuSerValGlyAlaII

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The invention describes isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynucleotide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; at sequence that hybridise to any of the nucleotide sequences under highly the above nucleotide sequences; or degenerate variants of the above nucleotide sequences. The composition and methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence encoded by a human lung tumour CDNA isolated from a lung squamous cell carcinome that may be useful in the diagnosis and treatment of lung cancer and
                                                                           New isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer.
                                                                                                                                                 Example 2; Page 249-251; 296pp; English.
  2003-540798/51,
  WPI; 2003-540798,
N-PSDB; ADA28437
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579 AA; Sequence

03-JAN-2002

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|ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
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                                                                                                                                                                                                                                                                                                                           The present invention describes human lung tumour proteins. Human lung activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polymucleotides, and can be used in vaccine production. Compositions proteins, T cell populations, or antigen presenting cells that express proteins, T cell populations, or antigen presenting cells that express stimulating an immune response. ABL48559 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
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                                                                                                                                                                      Henderson RA;
Fanger GR;
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Fanger N, Retter MW, Marnerakis M,
Carter D, Watanabe Y, Peckham DW;
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                                                                                                                                                                                                                                                                                                      Claim 2; Page 354-355; 374pp; English.
                                    28-JUN-2000; 2000US-00606421.
02-AUG-2000; 2000US-00630940.
21-AUG-2000; 2000US-0064597.
15-SEP-2000; 2000US-00662786.
09-OCT-2000; 2000US-00685696.
12-DEC-2000; 2000US-00685696.
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1639.00
83.89%
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            2001WO-US021065
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N-PSDB; ABL49283.
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Mcneill E
Vedvick 1
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The present invention describes isolated human lung carcinoma polypeptides (II) (I) and (II) have cytostatic polymucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polymucleotide that hybridises to the oligonucleotide and comparing the predecermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ2218 to ABQ32186 to ABBQ2186 and ABBC1866 to ABBC1862 represent sequences used in the exemplification of the present
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Retter MW, Durham M, Fanger GR, Vedvick TS;
Peckham DW, Cai F, Foy TM;
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                                                                                            cancer; lung tumour; cytostatic; gene therapy; vaccine
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                                 Human lung cancer associated protein sequence SEQ ID NO:427
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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D, Watanabe Y,
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Best Local Similarity:
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Conservative:
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  A.
  Sequence 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes isolated polynuclectides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung deancer. A new isolated polynuclectide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above, at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences cuted above; the above nucleotide sequences that is at least 75 or 90% identical to the above nucleotide sequences; or degenerate variants of the above nucleotide sequences; or degenerate variants of the above nucleotide sequences; or the amount methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence of a recombinant human lung tumour associated protein.
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nger GR, Vedvick
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PD, Fanger N, Retter MW, Durham M, Fanger GR,
), Watanabe Y, Peckham DW, Cai F, Foy TM;
                                          AAGGGA---CAGAGTAACCAGGCCCAGGCACGGAGGAAG 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotides and polypeptides useful preventing and/or treating cancer, particularly lung
                                                                                                                                                                                                                            cancer; lung cancer; gene therapy; vaccine; human; lung squamous cell carcinoma.
                                                         Recombinant human lung tumour protein L523S.
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                                                                                                                       ADA28517 standard; protein; 586
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98US-00123112.
98US-00221107.
99US-0028479.
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ATTATTGGCAAGGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATA 322
which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting development of cancer
                                                                                                                                                                                                                                                        CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCC
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GInThrProAspGluAsnAspGlnValValVallysIleThrGlyHisPheTyrAlaCys
                                CCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCT
                                            CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAAGTG
                                                                                    AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT
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|IysAlaLeuGlnSerGlyProProGlnSerArgArgLys 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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17-DEC-1999; 99US-00466396.
30-DEC-1999; 99US-0046496.
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protein is used for d
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N-PSDB; AAC65900.
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                                         507 GlybysThrValAsnGluLeuGlnAsnLeuSerSerAlaGluValValValProArgAsp 526
             390 ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
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Search completed: July 13, 2004, 12:08:40 Job time : 108 secs

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RESULT 1
US-09-261-655-2
US-09-261-655-2

Paquence 2, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILES REFERENCE: 960295-9313.1
CURRENT APPLICATION NUMBER: US/09/261,855A
NUMBER OF SEQ ID NOS: 46
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
IENCRITH: 577
TYPE: PRT
TYPE: PRT
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US-09-261-855-2
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Sequence 8, Appli
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Sequence 11, Appl
                                                                       July 13, 2004, 12:07:12; Search time 22 Seconds (without alignments) 8016.105 Million cell updates/sec
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11. /Ggn2_6/ptodarca/2/iaa/5A_COMB.pep:*
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16. /Ggn2_6/ptodarca/2/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-480-884A-176
US-09-542-615A-176
US-09-60-421B-176
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US-08-726-160-10
US-08-726-160-10
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Listing first 45 summaries
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                  AspGlnVall1eValLysIleIleGlyHisPheTyrAlaSerGlnMetAlaGlnArgLys
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Raios, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Lisamel Aljun
APPLICANT: Lisamel Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mand, Aljun
APPLICANT: Mandil, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210.11.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
CURRENT FILING DATE: 2000-08-21
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 2003-08-21
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Matches:
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US-09-643-597-348
; Sequence 348, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: Wang, Tongtong
APPLICANT: Ran, inquin
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chattanya S.
APPLICANT: Bangur, Chattanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPCUNDS AND METHODS FOF
TITLE REFERENCE: 210121 455C8
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-348
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Pred. No.:
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US-09-542-615A-348
; Sequence 348, Application US/09542615A
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Conservative:
Mismatches:
Indels: US-09-270-437D-5 (1-1708) x US-09-542-615A-348 (1-579) 4.72e-146 1639.00 83.89% 74.17% 52.70% Score:
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GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Ralos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Bosken, Mancy
APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Seels, Yasir A.W.

APPLICANT: Skelky, Yasir A.W.

APPLICANT: OMPOSITION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND APPLICANT: Skelky, Yasir A.W.

TITLE OF INVENTION: LONGOSITIONS AND APPLICANT: SCORPER AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9

CURRENT FILING DATE: 2000-06-28

CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 348

LENGTH: 579
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                               AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT
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LysbeugluAlaHisIleArgValProSerPheAlaAlaGlyArgValIleGlyLysGly
                                                                                                                                                                                                                                 GGAAAAACGGTGAACGAGTTGCAGAATTTGACGCCAGCTGAGGTGGTAGTACCAAGAGAC
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                                                                                                                                                                                                                                                                                     CAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGT
                                                                                                                                                                                                                                                                                                       GInThrProAspGluAsnAspGlnValValValVallySIleThrGlyHisPheTyrAlaCys
                                                                                                                      CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG
                                                                  CCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCT
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Raios, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Briger, A.W.
APPLICANT: McNeill Dariola D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERBNCE: 210121.455211
CURRENT FILING DATE: 2000-08-21
CURRENT FILING DATE: 2000-08-21
CURRENT FILING DATE: 2000-08-21
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
LENGTH: 579
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|IysAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 176, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
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1637.00
83.66%
74.17%
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CORGANISM: Homo sapiens
US-09-643-597-176
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Best Local Similarity:
Query Match:
DB:
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US-09-643-597-176
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Pred. No.:
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1087 AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT 1147 486 466 CCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCT GlnGlyArg11eTyrGlyLys11eLysGluGluAsnPheValSerProLysGluGluVal 1028 CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG 1088 ò

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CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCC

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.06 Db 230 AspValHisArgLysGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerTh	1207 Qy 383 CTGAGGCTGCTCCTCGCTTGTAGATGATCTTGGAGATTATGCATAAAGAGCTAAG 	.267 Qy 443 GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAAACTTTGTAGGG	24 Qy 503 C	OY 563 ATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGGGACCATCACTGTG	Oy 623 AAGGGGCCATCGAGAATTGTTGCAGGACCGAGGAAATAATGAAAAAGTTCGGGAG	Qy 683 GCCTATGAGAATGAGGCTGCCATGAGCTCTCACCTGATCCTGGCCTGAAC :::	Oy 737 CTGGCTGCTGTAGGTCTTTTCCCAGCTTCAGCGCAGTCCCGCCGCCT	Qy 788 CCCAGCAGCAGCGTTACTGGGGCTCCCTATAGCTGCAGGCTCCCGAGCAGGCAG	Qy 848 ATGGTGCAGGTGTTTATCCCCGCCCAGGCAGGGCAGAAAAGGGGCAG	Oy 908 CACATCAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCGGAAACA	968	Qy 1028 CAGGGAAGAATCTATGGCAAACTCAAGGAGAAACTTCTTTGGTCCCAAGGAAGG	Qy 1088 Db 487	.52 Qy 1148 GGAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTAGTACCAAGAGACGCAGCAGCAGCAGCTGAAGTACCAAGAGACGCAGCAGCAGCAGCAGCAGCAGCAGGCAG	Oy 1208 CAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATGGGACATTTCTATGCCAGT	1268 CAGAIGGCICAACGGAAGAICCGAGACAICCIGGCCCAGGTIAAGCAGCAGCAICAG	09 1325 AAGGGACAGAGTAACCAGGCACGAGGAAGG 1360	
	1148 GGAAAAACGGTGAACGAGTTGCAGAATTTGACGGAGCTGAGGTGGTAGTACCAAGAGAC 120 	1208 CAGACCCTGAIGAGAACGACCACGTCATCGTGAAAATCATCGGACATTTCTAIGCCAGT 126	1268 CAGATGGCTCAACGGAAGATCCGAGCTCTGGCCCAGGTTAAGCAGCAGCATCAG 132	1325 AAGGGACAGAGTAACCAGGCCCAGGGAAGGAAG 1360 	RESULT 6 US-09-480-884A-176 ; Sequence 176, Application US/09480884A	Patent No. 6482597 GENERAL INFORMATION: APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun	APPLICANT: Hosken, Nancy A. APPLICANT: Kalos, Michael D. APPLICANT: Fanger, Gary R. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY	TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 20121.455CG CURRENT APPLICATION NUMBER: US/19/480,884A CURRENT FILING DATE: 2001-08-27	MBER OF SEQ ID NOS: 330 PFWARE: FastSEQ for Windows Version 3.0 ID NO 176 ENGTH: 579	TYPE: PRT ORGANISM: Homo sapiens -09-480-884A-176	Alignment Scores: 7.3e-146 Length: 579 Pred. No.: 1637.00 Matches: 336 Percent Similarity: 83.66\$ Conservative: 43	74.17% Mismatches: 52.64% Indels: 4 Gaps:	D-5 (1-1708) x US-09-480-884A-176 (1-579) CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCTGAAGGTCTCC 91	ArgGlnAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysValAla 15 TACATCCCCGATGAGCAGATAGCACAGGGACTGAGAATGGGGGGGGGG	TyrileProAspGluMetAlaAlaGlnGlnAsnProLeuGlnGlnProArgGlyArgArg 17 GGCTTTGGCTCTCGGGGTCAGCCCGCCAGGGCTCACCTGTGGCAGCGGGGGGCCCCAGCC 20	ANGCAGCAGCAAGCATCCCCTTCGGCTCCTGGTGCCCCACCCA	LysGinLysProCybaSpleuProLeuArgleuLeuValProInFdInFheValGLyAla 2 ATTATTGGCAAGGAGGGCCACCATCGCAAAACACAAAACAGACCCAGTCCAAGATA 3 ATTATTGGCAAGGAGGGGCCACCATCAGAAACAGACAAAACAGACCCAGTCCAAGATA 3 ATTATTGTTGTTTGTTTTTTTTTTTTTTTTTTTTTTTT	77

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1028 CAGGGAAGAATCTAIGGCAAACICAAGGAGGAGAACTICTITGGICCCAAGGAGGAAGIG 1087
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                                         736
                                                                        350 SerTyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsn 369
                                                                                                                                    847
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                                                                                                                                                                                                                                                                                                                                    908 CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCACGAAACA 967
                                                                                                                                                                                                                                                                                                                                                       447 ProAspAlaLysValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAla 466
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   330 LysGlyAsnValGluThrCysAlaLysAlaGluGluGluIleMetLysLysIleArgGlu 349
                                                                                                                                                                                                                                                             848 ATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCATCATCGGCAAGAAGAAGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTATGAGAATGATGTGGCTGCCATGAGC - - - - TCTCACCTGATCCCTGGCCTGAAC
                                                                                                               CTGGCTGTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCG------CCT
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APPLICANT: Wang, Tongtong
APPLICANT: Ren, Ligun
APPLICANT: Ren, Ligun
APPLICANT: Rangur. Chaitanya S.
APPLICANT: Rangur. Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Panger, Gary R.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REPRENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1325 AAGGGA---CAGAGTAACCAGGCCCAGGCACGGAGGAAG 1360
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Patent No. 6518256;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fan, Liqua
APPLICANT: Fan, Liqua
APPLICANT: Fanger, Cary R.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Cary R.
TITLE OF INVENTION: CAPPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                              579
336
43
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Matches:
Conservative:
Mismatches:
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74.17%
52.64%
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US-09-542-615A-176
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                      908 CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCGGAAACA
                                             CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG
                                                                                                                                                                                                                                                        AAGCTGGAGACCCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT
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                                                                                                 CCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCT
                                                                                                                                                                                                  1325 AAGGGA---CAGAGTAACCAGGCCCCAGGCACGGAGGAAG 1360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVICAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZUP: 10154
ZUP: 10154
ZUP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFEOT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-021-608D-10; Sequence 10, Application US/08021608D; Patent No. 5580760
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ATTORNEY/ACENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 643
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: NEW YORK
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STATE: NE
COUNTRY:
ZIP: 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTATTGGCAAGGAGGCCACCATCGGCAACATCACAAAACAGACCCAGTCCAAGATA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 IleIleGlyLysGluGlyAlaThrIleArgAsnIleThrLysGlnThrGlnSerLysIle 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 IleThrIleSerProLeuGlnGluLeuThrLeuTyrAsnProGluArgThrIleThrVal 329
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|LeuAsnAlaLeuGlyLeuPheProProThrSerGlyMetProProProThrSerGlyPro 389
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390 ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
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190 LysGlnLysProCysAspLeuProLeuArgLeuLeuValProThrGlnPheValGlyAla
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                                                                                                                                                                                                                                                                                                                                                   92 TACATCCCCGATGAGCAGATAGCA---CAGGGACCTGAGAATGGGCGCCGAGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 143 GGCTTTGGCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGGGCCCCAACC
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                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                             7.3e-146
1637.00
83.66%
74.17%
52.64%
                  ORGANISM: Homo sapiens
                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                                  Percent Similarity:
Best Local Similari
                      ; ORGANISM: HOMO
US-09-606-421B-176
                                                                          Alignment Scores:
Pred. No.:
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------GGAAGAATCTATGGCAAACTCAAGGAGGAG 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1651 AAGAGGGTGGATCACACC-----TCAGTGGGAAGAAAATA 1686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1414 AGAGTGTGCTCCCCCCCCCGCAGGCCTGAGAATGAGTGGGGAATCCGGGACACNTGGGCCGGG 1473
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                                                                                                                                                                                                   310 PheLysProAspAspGlyThrThrProGlu-----ArglleAlaGln1leThrGly 326
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|IeGlyArgAsnGlyGluMetlleLySLysIleGlnAsnAspAlaGlyValArgIleGln 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::|||||||:::|||| 577 GlyGlnValAspTyrThrLysAlaTrpGluGluTyrTyrLysLysMetGlyGlnAlaVal 596
                                                                                                                                                                                                                                                                                                                                                  347 AlaGlyAsnProGlyGlyProGlyProGlyGryGglyArgGlyArgGlyArgGlyGlyGlyAsn
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367 TrpAsnMetGlyProProGlyGlyLeuGln---GluPheAsnPheIleValProThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 CAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCCATC
                                                                  --AsnGluGly11eAspValPro11eProArgPheAlaValGly11eVal
                                                                                                           ATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAG
                                                                                                                                                                                 ATTGCACCCGGAA----ACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGA
                                                                                                                                                                                                                                                                                     ProproAspArgCysGlnHisAlaAlaGluIleIleThrAspLeuLeuArgSerValGln
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503 roTyrAlaProGlnGlyTrpGlyAsnAlaTyrProHisTrpGlnGlnGlnAlaProProA
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| GlnProProAlaAlaProAlaGlyAlaProThrThrThrGlnThrAsnGlyGlnGly
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       ----SerArg1leGlyGly---
                                                                                                                                                                                                                                                     CCGCCAGAG---GCCCAATTCAAGGCTCAG----
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| GlyGlyGluGlnIleSerArgIleGlnGlnGluSerGlyCysLysIleGlnIle---Ala 136
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| ProAspAlaLysLysValAla------ProGlnAsn------AspSerPheGlyThr
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                                                                                                                                                                               Met or Ile
                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                      US-09-270-437D-5 (1-1708) x US-08-021-608D-10 (1-643)
                                                                                                                                                                               Amino Acid 148 (Xaa) is
                                                                                                                                                                                                                                                    Length:
Matches:
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnLeuProProMetHis---
                                                                                                                                                                                                                                              1.15e-14
248.50
37.80%
22.33%
7.99%
                                                                                                                                        FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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US-08-021-608D-10
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155 CGGGGTCAGCCCCGCCAGGCTCACCTGTGGCAGCGGGGGCCCCCAGCCAAGCAGCAGCAGCAA 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 SerValMetThrGluGluTyrLysValProAspGlyMetValGlyPheIleIleGlyArg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 GAGGGGCCACCATCCGCAACAICACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 GlyGlyGluGlnIleSerArgileGlnGlnGluSerGlyCysLysIleGlnIle---Ala 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 AAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAA------GAGGCTAAGGACACC 448
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157 GlnSerAlaLysArgLeuLeuAspGlnIleValGluLysGlyArgProAlaProGlyPhe 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 CCCGAT---GAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGCTTTGGCTCT 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
IDBUTIFICATION METHOD:
OTHER INFORMATION:
Amino Acid 148 (Xaa) is Met or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-270-437D-5 (1-1708) x PCT-US94-01782-10 (1-643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
             FILING DATE: 22-FEB-1994
CLASSIFICATION:
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
ATTOKNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET WUMBER: 26,728
TELECHONNICATION INFORMATION:
TELECHONE: (212) 758-4800
TELECHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 GlnLeuProProMetHis-------
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      PCT/US94/01782
                                                                                                                                                                                                                                                                                                                                                                                                             Peptide/Protein
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248.50
37.80%
22.33%
                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
STRANDENNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/P
HYPOTHETICAL: No
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE:
CELL TYPE:
CELL LINE: HL60
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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PCT-US94-01782-10
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                                            1181 GCAGCTGAGGTGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTC---ATC 1237
                                                                                                                             1238 GTGAAAATCATCGGACAT-----TTCTATGCCAGTCAGATGGCTCAACGGAAG 1285
                                                                                                                                                                                                              1286 AT-----CCGAGACATCCT---GGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAG 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- CAACAACGGCAGAAATCG 1413
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                                                                                                                                                      426 PheThrileArgGlyThrProGlnGlnIleAspTyrAlaArgGlnLeulleGluGluLys 445
                                                                                                                                                                                                                                                         464
                                                                                406 GlyAlaArgIleGluLeuGlnArgAsnProProProAsnAlaAspProAsnMetLysLeu 425
                                                                                                                                                                                                                                                                                                                              465 ---ProGlyPro--HisGlyProProGlyProProGlyProGlyThrProMetGlyProT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |||||:::||| : 503 roTyrAlaProGlnGlyTrpGlyAsnAlaTyrProHisTrpGlnGlnGlnGlnAlaProProA 523
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569 Asp------GinglnAsnProAlaProAla 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 GlnProProProAlaAlaProAlaGlyAlaProThrThrThrGlnThrAsnGlyGlnGly 568
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LysThrGlyLeuIleIleGlyLysGlyGlyGluThrIleLysSerIleSerGlnGlnSer 405
                                                                                                                                                                                                                                         1336 TAACCAGGCCCAGGCACGGA------GGAAGTGACCAGCCCTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::|||||||
539 Tyr-----TyrAlaHisTyrTyrGlnGlnAla-----TyrAlaHisTyrTyrGlnGlnGlnAla
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| Sequence 10, Application PC/TUS9401782
| Sequence 10, Application PC/TUS9401782
| GENERAL INFORMATION:
| APPLICANT: THE GOVERNMENT OF THE UNITED STATES
| APPLICANT: HEALTH AND HUMAN SERVICES
| TITLE OF INVENTION: NOVEL FUSE BINDING
| TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
| TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MORGAN & FINNEGAN
| STREET: 345 PARK AVENUE
| COUNTRY: NEW YORK
| COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFEGT 5.1
CURRENT APPLICATION DATA:
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ProAlaProThrGly 601
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	Qy 1651 AAGAGGGTGGATCACCTCAGTGGGAAGAAATA 1686 Sin	gth: 49 servative: 49 matches: 0 els: 0 is: 0 is: 0 is: 149) ig: (1-49) ig:	Oy 536 AAGTAGACAATACCAGACAAAATCACCATCTCTTGCAGACCTTACCTT 595
AAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTA 49	268	3lyasn 3CATCA ThrGly TTGACG ::: 3lnSerATC LysLeu CGGAAG	1286 ATCCGAGACATCCTGGCCCAGGTTAAGCAGCATCAGAAGGACAGAG 1335 446 IleGlyGlyProValAsnProLeuGlyProProValProHisGlyProHisGlyVal 464 1336 TAACCAGGCCCAGGCACGAAGGAAGTGACCAGCCCTC 1373

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GAGGAAGTGAAGCTGGAGACCCACATACGTGCCCACATCAGCAGCTGGCCGGGTCATT 1138
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317 ThrThrProGlu-----ArgIleAlaGlnIleThrGlyProProAspArgCysGln 333
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334 HisAlaAlaGluIleIleThrAspLeuLeuArgSerValGlnAlaGlyAsnProGlyGly 353
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238 ThrdlyAspFroTyrLysValGlnGlnAlaLysGluMetValLeuGluLeuIleArgAsp 257
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222 IleGlnAsp------GlyProGlnAsnThrGlyAlaAspLysProLeuArgIle 237
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          ---GCCCCAGCCAAGCAGCAGCAAGTGGACATCCCCCTT-----CGG 232
                                                         85 PheGlyThrGlnLeuProProMetHisGlnGlnGlnSerArgSerValMetThrGluGlu 104
                                                                                                                                           105 TyrLysValProAspGlyMetValGlyPhellelleGlyArgGlyGlyGluGlnlleSer 124
                                                                                                                                                                                                               353 GCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGCTCCTCCGCTTGTAAGATG 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .---- 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
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---ProLeuGluAspGlyAspGlnProAspAlaLysLysValAlaProGlnAsnAspSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 AACCATGCCCTGAAGGTCTCCTACATCCCCGATGAGCAGATAGCACAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Amino Acid 149 (Xaa) is Met or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 TCACCTGTGGCAGCGGGG------
Sequence 2, Application US/08021608D
Patent No. 5580760
GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
ITLE OF INVENTION: NOVEL FUSE BINDING
ITLE OF INVENTION: NOVEL FUSE BINDING
ITLE OF INVENTION: PROTEIN AND CDNA THEREFOR NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: ADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                      24
.. ANI
24
.. ANI
21RET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USP
ZIP: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: Single
TOPPLOGY: Unknown
MOLEULE TYPE: Peptide/Protein
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 20.
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245.00
36.46%
22.39%
7.88%
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL LINE: HL60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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Query Match:
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1139 GGCAAAGGTGGAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTA 1198
                                                                                                                                                   ------TTCTATGCCAGTCAGATGGCTCAACGGAAGAT------CCGAGACAT 1296
                                                                                                                                                                                                                                                                                                     GA-----CCTGTCCCTTNGA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAATTGGC---CCAACACTGTNTGCCCCTCGGGGTGTCAGAAATTNTAGCGCAAGGCAC 1608
                                                                                                                                                                                                                         CCT----GGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGGCACG 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------CAACAACGGCAGAATCGAGGTGTGCTCTCCCCCGG 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1432 CAGGCCTGAGAATGAGTGGGAAATCCGGGACACNTGGGCCGGCTGTAGATCAGGTTTGCC 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1609 TITTAAACGTGGATTGTTTAAAGAAGCTCTCCAGGCCCCCACCAAGAGGGTGGATCACACC 1668
                       413 GlnArgAsnProProProAsnAlaAspProAsnMetLysLeuPheThr1leArgGlyThr 432
                                                                                                                                                                             433 ProGlnGlnIleAspTyrAlaArgGlnLeuIleGluGluLysIleGlyGlyProValAsn 452
                                                                                                                                                                                                                                                       453 ProLeuGlyProProValProHisGlyProHisGlyVal-----ProGlyPro--HisG 470
                                                                                                                                                                                                                                                                                                                                 470 lyProProGlyProProGlyProGlyThrProMetGlyProTyrAsnProAlaProTyrA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1492 CACTTGATTGAGAAAGATGTTCCAGTGAGGAACCCTGATCTNTCAGCCCCCAAACACCCCAC 1551
                                                                                                                                                                                                                                                                                                                                                                                                                 490 snProglyProProglyProAlaProHisGlyProProAlaProTyrAlaProGlnGlyT 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ProA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526 laLysAlaGlyThrAspProAsnSerAla-AlaTrpAlaAlaTyr-----TyrAla 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProAladiyAlaProThrThrThrGlnThrAsnGlyGlnGlyAsp------ 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TCAGTGGGAAGAAAAAAATTTCCTTCAGGT 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1199 CCAAGAGACCAGACCCTGATGAGAACGACCAGGTC---ATCGTGAAAATCATCGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-726-160-2
Sequence 2, Application US/08726160
Patent No. 5/34016
GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
TITLE OF INVENTION:
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
TITLE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 1015-4

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 PARK AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 AACCATGCCCTGAAGGTCTCCTACATCCCCGATGAGCAGATAGCACAG------GGACCT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 PheGlyThrGlnLeuProProMetHisGlnGlnGlnSerArgSerValMetThrGluGlu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 CTCCTGGTGCCCACCCAGTATGTGGGTGCCATTATTGGCAAGGAGGGGGCCACCATCCGC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrLysValProAspGlyMetValGlyPhelleIleGlyArgGlyGlyGluGlnIleSer 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ArgileGlnGlnGluSerGlyCysLysileGlnIle---AlaProAspSerGlyGlyLeu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGCTCCTCCGCTTGTAAGATG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAAG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ProLeuGluAspGlyAspGlnProAspAlaLysLysValAlaProGlnAsnAspSer 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 AsnAspAlaPheLysAspAlaLeuGlnArgAlaArgGinileAlaAlaLysIleGlyGly 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 ------GCCCCAGCCAAGCAGCAGCAGTGGACATCCCCCTT-----CGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 ATCTTGGAGATTATGCATAAA-----GAGGCTAAGGACACCAAAACGGCTGAC----
                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION: Amino Acid 149 (Xaa) is Met or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644
148
93
202
33
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Conservative:
Mismatches:
Indels:
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                          FILING DATE: ...

CLASSIFICATION: 435
ATTONEY/ABBAY INVENDATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 26,728
REPERENCE/POCKET NUMBER: 2026-4063US1
FELEPHONE: (212) 758-4800
FILEPRAXION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644
TYPE: Amino Acid
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,608
FILING DATE: 22-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 TCACCTGTGGCAGCGGGG----
                                                                                                                                                                                                                                                            STRANDEDNESS: Single
TOPLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
HYPOTHETICAL: No
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245.00
36.46%
7.88%
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                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: 1
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HAPLOTYPE:	Db 258 GlnGlyGlyPheArg(GlnGlyGlyPheArgGluValArgAsnGluTyrGly 269
TISSUE TYPE:	Qy 728 GGCCTGAACCTGGCTG	GGCCTGAACCTGGTGTTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGTCCCGGCGGCT 787
CELL LINE: HL60 COUNTRY HL60 COUNTRY HL60	Db 269	598
FALLKE: NAMBYKEY: LOCATION:	788	GCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAG
; IDENTIFICATION METHOD: ; OTHER INFORMATION: ; OTHER INFORMATION: Amino Acid 149 (Xaa) is Met or 11e	Db 270SerArgileGlY(GLYASNGLU Z/6 ATCCCGCCCAGGCAGTGGGCGCCATCATCGGCAAGAAGGGGCAG 907
01782-2	277	GlylleAspValProlleProArgPheAlaValGlylleValIleGlyArgAsnGlyGlu 296
4.	Qy 908 CACATCAAACAGCTC	CACATCAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCGAA 964
t Similarity: 36.46\$ Conservative:	Db 297 MetileLysLysileC	::::
. 7.88% . S. 88%	965	ACACCTGACTCCAAAGTTCGTATGTTATCACTGGACCGCCAAGGCCCAA 1018
US-09-270-437D-5 (1-1708) x PCT-US94-01782-2 (1-644)	317	
Oy 71 AACCATGCCTGAAGGTCTCCTACATCCCCGATGAGGAGATAGCACAGGGACCT 124	<pre>Qy 1019 TICAAGGCICAG Db 334 HisAlaAlaGluIlel</pre>	TTCAAGGCTCAG 1030 ::: HisAlaAlaGluIleIleThrAspLeuLeuArgSerValGlnAlaGlyAsnProGlyGly 353
125 GAGAATGGGCGCCGAGGGGGTTTGGCTCTCGGGGTCAGCCCCGCCAGGGC	Qy 1031GGA	GGAAGAATCTAIGGCAAACTCAAGAGAGAGAACTTCTTTGGTCCCAAG 1078
::: 48 AspAlaGlyThrSerL	354	
Qy 176 TCACCTGTGGCAGGGGG	Oy 1079 GAGGAAGTGAAGCTGG :::::: Db 374 GlvGlvLeuGlnC	GAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATT 1138
66ProLeuGluAspGlyAspGlnProAspAlaLysLysValAlaProGlnAsnAspSer	1139	
Qy 194GGCCCAGCCAAGCAGCAGCAGCAGCAGCACTCCCCTTCGG 232	393	::: :::
233 CTCCTGGTGCCCACCAGTATGTGGGGCCATTATTGGCAAGGGGGGCCACCATCGGC	Qy 1199 CCAAGAGACCAGACCC	
105 TyrLysValProAspGlyMetValGlyPheileileGlyArgGlyGluGlnIleSer	413 GlnArgAsnP	
Qy 293 AACATCACAAAAACCGACCCAGTCCAAGATAGACGTGCATAGGAAGGA	Qy 1256TTCT Db 433 ProGlnGlnIleAsp	TTTTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACAT 1296
Db 125 ArgiledlnGluSerGlyCysLysIledlnIleAlaProAspSerGlydlyLeu 143	1297	
Qy 353 GCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGCTCCGCTTGTAAGATG 412	453	
413 ATCTTGGAGTTATGCATAAGAGGCTAAGGACACCAAAACGGCTGAC	1354	GAGGAAGTGACCAGCCCTCCCTGTCCCTTNGA 1386
Db 164 LeuAspGlnIleValGluLysGlyArgProAlaProGlyPheHisHisGlyAspGlyPro 183	DD 4/O INFICKIONING DD OF THE THE DD OF THE THE DD OF THE	FOGLYFFOGLYIMFFOMENCLFFFOLYIMFLOMIAFICLFF #90
OY 461GAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAAG 517	490	snProGlyProProGlyProAlaProHisGlyProProAlaProTyrAlaProGlnGlyT 510
104 017 017 017 017 017 017 017 017 017 017	1395	AGTGTGCTCTCCCCGG
204 GlyGluThrIleLysGlnLeuGlnGluArgAlaGlyValLysMetValMet	510	
578 TIGGAAGACCTTACCACCTGAGAGGACCATCACTGTG :::	Qy 1432 CAGGCCTGAGAATGAG 	CAGGCCTGAGAATGGGAATCCGGGGACA.NTGGCCGGGGTGTAGATCAGGTTGGC 1491
Db 222 IleGlnAspGlyProGlnAsnThrGlyAlaAspLysProLeuArgile 237	Qy 1492 CACTTGATTGAGAAAG	CACTIGAITGAGAAAGAIGITCCAGIGAGGAACCCIGAICINICAGCCCCAAACACCCAC 1551
238 ThrGlyAspProTyrLysValGlnGlnAlaLysGluMetValLeuGluLeuIleArgAsp	543	3lnAlaGlnProProProAlaAla 555
Qy 683GCCTATGAGAATGATGTGGCTGCCATGAGCTCTCACCTGATCCCT 727	Qy 1552 CCAATTGGCCCAR 556 ProAlaGlyAlaProI	CCAATTGGCCCAACACTGTNTGCCCCTCGGGGTGTCAGAAATTNTAGCGCAAGGCAC 1608

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Sequence 5, Application US/09061709B
; Sequence 5, Application US/09061709B
; Patent No. 6297364
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Stockert, Ali
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Much, Alexander
; APPLICANT: Much, Alexander
; APPLICANT: Much, Alexander
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; TITLE CT INVENTION NUMBER: US/09/061,709B
; CURRENT APPLICATION NUMBER: US/09/061,709B
; CURRENT FILING DATE: 1998-04-17
Sequence 75, Appl Sequence 11, Appl Sequence 17202, A Sequence 6251, Ap Sequence 6339, Ap Sequence 6131, Ap Sequence 175, Ap Sequence 15639, Ap Sequence 183, Appl Sequence 2813, App Sequence 2813, App Sequence 2813, App Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli
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US-09-61-99A-375
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US-09-070-356-1
US-09-070-356-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1708; Conservative 0; Mismatches
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  TYPE: DNA
ORGANISM: Homo sapiens
  SEQ ID NO 5
LENGTH: 1708
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Sequence 8, Appli
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Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 175, Appli
Sequence 5, Appli
                                                                              July 13, 2004, 17:54:49; Search time 134 Seconds (without alignments) 7073.553 Million cell updates/sec
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

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(c) 1993 - 2004 Compugen Ltd.
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                                                           nucleic search, using sw model
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QY 1410 ATCGAGAGTGTCTCCCCGGCAGGCCTGAGAATGGGAATCCGGGACACNTGGGC 1469 Db 1648 ATCGAGAGTGTCTCTCCCGGCAGGCCTGAGAATCCGGGACACNTGGGC 1707 QY 1470 CGGGCTGTAGATCAGGTTTGCCCACTTGATTGAGAAGTGTTCCAGTGAGGAACCTGA 1529 Db 1708 CGGGCTGTAGATCAGGTTTGCCCACTTGATTGAGAAGTGTTCCAGTGAGGAACCTGTA 1767 CY 1530 TCTNTCAGCCCAAACACCCACCACTGATTGGCCCAACACTGTNTGCCCTCGGGGTCCAG 1767 Db 1768 TCTNTCAGCCCAAACACCCACCACTGATTGGCCCAACACTGTNTGCCCTCGGGGTGTCAG 1829 CY 1590 AAATHNTAGCCCCAACACTGTTTAAAACGTGGATTGTTTAAAGAAGTTCTCCAGGCCCCAC 1840 Db 1828 AAATHNTAGCGCAAGGCACTTTTAAAACGTGGATTGTTTAAAGAAGCTCTCCAGGCCCCAC 1887 QY 1650 CAAGAGGGGATCACACCTCAGTGGAATTGTTTAAAAAATTTCCTTCAGGCCCCAC 1887 QY 1650 CAAGAGGGGATCACACCTCAGTGGGAATAAAAATAAAAT	RESULT 5 US-09-261-855-1 Sequence 1, Application US/09261855A Sequence 1, Application US/09261855A Sequence 1, Application US/09261855A Sequence 1, Application US/09261855A Sequence 1, Application US/0926185A Sequence 1, Application US-09-261 Sequence 1, Application US-09-261 Sequence 1, December 199-09-09 SEQUENCE INTERCOME (RD-BP) AND ITS NUCLEIC ACID SEQUENCE SIDE REPRENCE: 960295, 991331 CURRET APPLICATION NUMBER: US/09/261, 855A SEQUENCE PARAMETH: 2244 SEQUENCE PARAMETH: 2244 SEQUENCE: 199-03-03 SEQUENCE: DAW SEQUENCE: 2.0	
330 ATAGGAAGGAGAACCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGG 389 568 ATAGGAAGGAACGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGG 389 568 ATAGGAAGGAACGCAGCTGCAGCTGCACTCCAGTGTGCACTCCACCCCTGAGG 627 390 GCTGCTCCTCCGCTTGTAAGATGCTTGGAGATTATGCATAAAGAGCCTAAGGACACCA 449 628 GCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGCCTAAGGACACCA 687 450 AAACGGCTGCTCCTGAAGATGATCTTGGAGATTATGCATAAAGAGCTAAGGACACCA 687 650 AAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGACACCA 687 650 AAACGGCTGAAGGATCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGCCGTCTCA 747 510 TTGGCAAGGATGCCTGAAGAATCCTGACCCCATAATAACTTTTGTAGGCGTTCCA 569 748 TTGGCAAGGACGGAACCTGAAGAAGCTGAAGAGAGCCAACAAAATCACCC 807 570 TCTCCTCGTTGCAAGACCTTAACAACCCTGAAGAGACCAACAACAAAAAAAA	CCATCGAGAATTGTTGCAGGGCCGAGAAGAATAATGAAGAAAGA	1290 GAGACATCCTGGCCCAGGTTAAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGG 1349

Db 2024 AGAACAATGTTCCAGTGAGAATCCTGATCTCTCGCCCCAATTGAGCCAGCTGGCCA 2081	Sequence 34', Application US/09643597 Sequence 34', Application US/09643597 Sequence 34', Application US/09643597 Sequence 34', Application US/09643597 Septicant No. 642607 Sensati INCORMATION: APPLICANT: Raios, Midnel D. APPLICANT: Raios, M	DD 582 TGATTIGCOLCIGGRACATCCCACCAATTIGTIGGRACATCATCATAGA 941 OY 277 GGGGCCACCATCGCAACATCACAAACAGACCAGTCCAAGATAGAGA 336 642 AGGGCCACCATTCGGAACATCACAAACAGCCCAGTCCAAGATGATGATGCTCCACCTAAAATCGCACCTAAAACAGAACGCAGCTGAAAACGCAGTCCAAGAACGCAGTTCAAAAAGCCAACATCAAAATCCACCCTGAGGCTGCTC 396 OY 337 GGAGAACGCAGGTGCAGAAAAAGCCATCACTCTACAACCCTGAGGCTGCTC 396 DD 702 AGAAAATGCGGGGGCTGCTGAAAAAGCCATTACTATCCTCTCTCT
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GACATGTGCCAAAGCTGAGGAGGAGATCATGAAGAAATCAGGGAGTCTTATGAAAATGA 1061
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                                 FOR THERAPY CANCER
                                                                                                                                                                                                                                                 34.1%; Score 582.2; DB 4; larity 66.2%; Pred. No. 2.8e-156; Conservative 0; Mismatches 433;
              APPLICANT: Fanger, Gary R...
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAR, FILE REPERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 347
   Nancy A.
                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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   Hosken,
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RESULT 7
US-09-542-615A-347
US-09-542-615A-347
Sequence 347, Application US/09542615A
Petent No. 651826
GENERAL INFORMATION:
APPLICANT: Mang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.

TCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGCTGCAGGTGTTATCCCCGC

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1182 TCCTCCCTACCCGCAGTTTGAGCAATCAGAAACGGAGACTGTTCATCTGTTTATCCCAGG 1241 871 CCAGGCAGTGGGCGACATCAGGCAAGAAGGGGCCAGCACTCAACAGCTCTCCCGGTT 930 1242 TCTATCAGTCGGTGCATCATCGGCAAGAGGGCCAGCAGCAGTCAAGCAGCTTTCTCGCTT 1301 931 TGCCAGGCCTCCATCAAGATTGCACCACCCGAAACAGCAGCAGTCCAAAGTTGGTAGGT 990 1302 TGCTGGAACTTCAATTAGAATTGCTCCAGGAAGATGGTTAAAGTGAAGATGGT 1361	TATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACT	1051 CAAGGAGAGAACTTCTTTGGTCCCAAGGAGGAAGCTGAGACCCCACATACGTGT 110	1171 GAATTTGACGGCAGCTGATAGTACCAAGAGCCAGACCCTGATGAGAACGACCA	1602 AGTGGTTGTCAAAATAACTGGTCACTTCTATGCTTGCCAGGGTTGCCCAGAGAAAATTCA 1661 1291 AGACATCCTGGCCCAGGTTAAGCAGCATCAGAAG 1327 1662 GGAAATTCTGACTCAGGTAAAGCAGCACAACAAG 1698	NESULT 8 US-09-606-421B-347 Sequence 347, Application US/09606421B Patent No. 6531315 SENERAL INFORMATION:	PELICANT: Mang, Tongroup PELICANT: Kalos, Michael D. PELICANT: Bangur, Chaitanya S. PELICANT: Borger, Gary R. PELICANT: Panger, Gary R. PELICANT: Fin, Samuel X. PELICANT: Wang, Aijun	HAPPLICANT: SKEALY, YESTE A.W. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REPRESENCE: 2.1012.1455C9 CURRENT APPLICATION NUMBER: US/09/606,421B CURRENT APPLICATION NUMBER: 2000-06-28 NUMBER OF SEQ ID NOS: 358 SOFTWARE: FESCUSEO for Windows Version 3.0	LENGTH: 1740 TYPE: DN A ORGANISM: Homo sapiens 5-09-606-421B-347	Ouery Match 34.1%; Score 582.2; DB 4; Length 1740; Best Local Similarity 66.2%; Pred. No. 2.8e-156; Matches 858; Conservative 0; Mismatches 433; Indels 6; Gaps 1; Matches 37 AGCCATCATGAAGCTGACCACAGTTGAGAACCATGCCTGAAGGTTCTCTACAT 96	402 AGCACTAGACAAACTGAATGGATTTCAGTTAGAGAATTTCACCTTGAAAGTAGCGTATAT 461 97 CCCCGATGAGCACACAGAGACCTGAGAATGGGGGGGGGG

1170 1121 1241 1301 1110 1361 CCCCAGAGGCCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACT 1050 TGGCAGAGTTATTGGAAAAGGAGCAAAACGGTGAATGAACTTCA 1541 CTGAGGAGGAGATCATGAAAATCAGGGAGTCTTATGAAATGA 1061 inginagicchaaagagagigaachtgaagchcanarcagagn 1481 216 336 989 decterataarceaeaacecactarracaetraaaeecaaretrea 1001 chrcaedeaneccacchccaechcaedececechrcaeceaneae 1181 930 990 276 641 456 516 IGAAGAAGGTAGAGGAAGATACCGAGACAAAAATCACCATCTCCTC 576 969 750 CATCCAGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTGC 810 870 CCTCAAGGCAGGGTCTCCAGGATCCGTATCCAAGCAGAACCATG 581 701 CAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGCTC 396 761 821 881 941 CIGCTGAGAAGTCGATACTACTCTTCTACTCCTGAAGGCACCTC GCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGGAA CTATICTGGAGATTATGCATAAGGAAGCTCAAGATATAAAATTCAC TTAAAAAATTGAGCAAGACACAGACACTAAAATCACGATATCTCC CATCATCGCCAAGCAGGCCAGCACATCAAGCAGCTTTCTCGCTT rcrirggrcccaaggaggaagrgaagcrggagacccacarargr AGGGCTCACCTGTGGCAGCGGGGCCCCAGCCAAGCAGCAGCAAGT GECTCCTGGTGCCCACCCAGTATGTGGGTGCCATTATTGGCAAGGA <u> eccieciredricceacceaririciredaecearcaradaaaaa</u> CCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGA -----GCTCTCACCTGATCCCTGGCCTGGACCTGGCTGCTGGG arcricaagcacarrraatrccrggarraaarcrgaacgccrrgg TOGCCOCGCTCATTCGCCAAAGGTGGAAAAACGGTGAACGAGTTGCA TGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAAACGGC TGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAA CCGACCAGGAAATAATGAAGAAGTTCGGGAGGCCTATGAGAATGA TTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGC CATCATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTT TCAAGATTGCACCCGAAACACCTGACTCCAAAGTTCGTATGGT

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Sequence 4, Application US/09899651
Sequence 4, Application US/09899651
Sequence 4. Application US/09899651
Sequence 4. Application US/09899651
Sequence 4. Application Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gue, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Solated Nucleic Acid Molecules Encoding Cancer;
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Antigen; The Antigens Per Se, And Uses Thereof
CURRENT APPLICATION UNBER: US/09/061,709
PRIOR APPLICATION NUMBER: US/09/061,709
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US-09-061-709-4

Second of Application US/09061709B

Patent No. 6297364

GENERAL INFORMATION:

APPLICANT: Tone, Yao-Tseng

APPLICANT: Stockert, Blisabeth

APPLICANT: Stockert, Blisabeth

APPLICANT: APPLICANT: All

APPLICANT: Jager, Elke

APPLICANT: Muth, Alexander

APPLICANT: Muth, Alexander

APPLICANT: Muth, Alexander

APPLICANT: Muth, Alexander

TILE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated

TILE OF INVENTION: Antigens Per Se, And Uses Thereof

TILE REPREBRICE: UND 5538

CURRENT APPLICATION NUMBER: US/09/061,709B

CURRENT FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 8
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                                                          1602 AGTGGTTGTCAAATAACTGGTCACTTCTATGCTTGCCAGGTTGCCCAGAAAAATTCA
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Pred. No. 1.2e-155;
0; Mismatches 434;
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Best Local Similarity 66.1%;
Matches 857; Conservative
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LENGTH: 4159
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Skeiky, Yasir A.W.

Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

TITLE OF INVENTION: Patricia D.

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REPERBREC: 210121.455C11

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21

SOFTWARE: FastSEQ for Window- .

SEQ ID NO 175

LENGTH: 4181

TYPE: DN?

OPPT: OPPT: DN?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 175, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
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Fan, Liqun
Kalos, Michael D.
Bangur, Chattanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
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LOCATION: (3347)
OTHER INFORMATION: N
NAME/KEY: unsure
LOCATION: (3502)
OTHER INFORMATION: N
NAME/KEY: unsure
LOCATION: (3506)
OTHER INFORMATION: N
NAME/KEY: unsure
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OTHER INFORMATION:
NAME/KEY: unsure
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OTHER INFORMATION:
NAME/KEY: unsure
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                                                                                                                                            Query Match 34.0%; Score 580.6; DB 4; Best Local Similarity 66.1%; Pred. No. 1.2e-155; Matches 857; Conservative 0; Mismatches 434;
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
LENGTH: 4159
                                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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US-09-899-651-4
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  TGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGGT
                                                                                             TATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACT
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Facture No. 6482537

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fanger, Marcy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILLING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 175
LENGTH: 4181
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Pred. No. 1.2e-155;
0; Mismatches 434;
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LOCATION: (4080)
OTHER INPORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4088)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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Best Local Similarity 66.1%;
Matches 857; Conservative
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OTHER INFORMATION: n
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LOCATION: (3974)
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NAME/KEY: unsure
LOCATION: (4056)
OTHER INFORMATION: n
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LOCATION: (4062)
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Sequence 175, Application US/09542615A

Patent No. 6518256

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Rangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS OF LUNG CANCER
TITLE OF ILLING DATE: 21012.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT PELING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1912 GGAAATTCTGACTCAGGTAAAGCAGCACCAACAACAG 1948
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FEATURE:
NAME/KEY: unsure
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OTHER INFORMATION: NAME/KEY: unsure
LOCATION: (3502)
OTHER INFORMATION: NAME/KEY: unsure
LOCATION: (3506)
OTHER INFORMATION: 0
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LOCATION: (3520)
OTHER INFORMATION: n
NAME/KEY: unsure
LOCATION: (3538)
OTHER INFORMATION: n
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LOCATION: (3549)
OTHER INFORMATION:
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US-09-542-615A-175
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                                                                                                                                                            Length 4181;
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                                                                                                                                                              Query Match 34.0%; Score 580.6; DB 4; Best Local Similarity 66.1%; Pred. No. 1.2e-155; Matches 857; Conservative 0; Mismatches 434;
      ; TYPE: DNA; ROGANISM: Homo sapiens; FEATURE: NAME/KEY: misc_feature; CATHER INFORMATION: (1)...(4181); OTHER INFORMATION: n=A,T,C or GUS-09-480-884A-175
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      GAATTTGTCAAGTGCAGAAGTTGTTGTCCCTCGTGACCAGACACCTGATGAGAATGACCA 1851
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Lidgun
APPLICANT: Fan, Lidgun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hanger, Chaitanya S.
APPLICANT: Hanger, Mancy
APPLICANT: Hanger, Mancy
APPLICANT: Hanger, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
ITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT FILING DATE: 2000-06-28
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFUTHER: FastESQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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US-09-606-421B-175
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Pred. No. 1.2e-155;
0; Mismatches 434;
                                                                                                                                                                                                                                                                                                                                                 | LOCATION: (4080)
| OTHER INFORMATION: n=A,T,C or G
| NAME/KEY: unsure
| LOCATION: (4088)
| OTHER INFORMATION: n=A,T,C or G
| NAME/KEY: unsure
| LOCATION: (4115)
| OTHER INFORMATION: n=A,T,C or G
| US-09-542-615A-175
                                                          LOCATION: (3968)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3974)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4036)
OTHER INFORMATION: n=A,T,C or G
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Best Local Similarity 66.1%;
Matches 857; Conservative
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OTHER INFORMATION: n=A,T,C or
NAME/KEY: unsure
LOCATION: (4062)
OTHER INFORMATION: n=A,T,C or
NAME/KEY: unsure
LOCATION: (3940)
OTHER INFORMATION: n=A,T,C
NAME/KEY: unsure
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FEATURE: NAME/KEY: unsure LOCATION: (3347) FOTHER INFORMATION: n=A,T,C or G	FABLORE: NAME/KEY: unsure LOCATION: (3502) OTHER INFORMATION: n=A,T,C or G	; FEATURE: ; NAME/KEY: unsure ; LOCATION: (3506) ; OTHER INFORMATION: n=A,T,C or G	; FEATURE: ; NAME/KEY: unsure ; LOCATION: (3520) ; CTHER INFORMATION: n=A,T,C or G) FEATURE:) NAME/KEY: unsure) LOCATION: (3538)) OTHER INFORMATION: n=A,T,C or G	FACALUKEY: unsure; COCATION: (3549) COTHER INFORMATION: n=A,T,C or G	NAME/KEY: unsure ; LOCATION: (3646) ; CHER INFORMATION: n=A,T,C or G	NEME/KEY: unsure LOCATION: (3940) 	; FEATURE: NAME/KEY: unsure ; LOCATION: (3968) ; OTHER INFORMATION: n=A,T,C or G	NAME/KEY: unsure ; LOCATION: (3974) ; OTHER INFORMATION: n=A,T,C or G	NAME/KEY: unsure) FEATURE:) NAME/KEY: unsure) LOCATION: (4056)); THER INFORMATION: n=A,T,C or G	FABLOKEY: Unsure; LOCATION: (4062) FORTHER INFORMATION: n=A,T,C or G) Fablus:) NAME/KEY: unsure) LOCATION: (4080)) OTHER INFORMATION: n=A,T,C or G	FARIUME: NAME/KEY: unsure LOCATION: (4088) FORTHER INFORMATION: n=A,T,C or G	FABLOKE: FABLOKE: FABLOKE: FOCATION: (4115) FOCATION: (4115) FOCATION: n=A,T,C or G	Juery Match 34.0%; Score 580.6; DB 4; Length 4181; 34.0%; Pred, No. 1.2e-155; 34.0%; Pred, No. 1.2e-155;	CONSELVACIVE CATCATGAAGCTGAAT

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                   517 GGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAATCACCATCTCCTC
                                                                                      GTTGCAAGACCTTACCCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCCATCGA
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Facent No. 6297364

GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng

APPLICANT: Stockert, Elisabeth

APPLICANT: Stockert, Elisabeth

APPLICANT: Gar, Solam

APPLICANT: Muth, Alexander

APPLICANT: Muth, Alexander

APPLICANT: Old, Lloyd 0.

TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof

FILE REPERBNCE: LUD 5538

CURRENT APPLICATION NUMBER: US/09/061,709B

CURRENT FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 8
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                                                                    GGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCG
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Pred. No. 8.4e-134;
0; Mismatches 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6%;
Matches 849; Conservative
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Pred. No. is the number of results predicted by chance to have a

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1 (bases 1 to 1708)

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4 (bar, Y. T., Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K. and Old, L.J.

Isolated mucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof

Patent: US 6576756-A 10-UN-2003,

Location/Qualifiers

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/organism="unknown"
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Isolated nucleic acid molecules encoding cancer-associated antigens, these antigens and method of using the same. BD20924. I GI:33019694 GF 2002512049-A/3. Home sapiens (human) Home sapiens (human)
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1 (bases 1 to 1708)
Chen, Y.T., Gure, A., Tsang, S., Stockert, E., Jager, E., Knuth, A. and Old, L.J.
Isolated nucleic acid molecules encoding cancer-associated antigens, these antigens and method of using the same patent: UP 2002512049-A 3 23-APR-2002; LUDMG INSTITUTE FOR CANCER RESEARCH
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PR 17-APR-1998 US 09/061709
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/moi_type="genomic DNA"
/db_xref="taxon:9606"
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DEFINITION Sequence 7 from patent US 6297364. ACCESSION AR171866 1:17910816 ACRINICAL AR171866.1 GI:17910816 SOURCE Unknown. ORGANISM Unclassified. I (bases 1 to 1946) AUTHORS Chen YT., Gure, A., Tsang, S., Stockert, E., Jager, B., Alexander, K. and Old, L.Y. TITLE Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof JOURNAL Patent: US 6297364. TITLE Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof JOURNAL Patent: US 6297364.A 7 02-OCT-2001; FEATURES 1. 1946 //ORGANISM Mol_type="unassigned DNA"	Query Match 97.7%; Score 1669.2; DB 6; Length 1946; Best Local Similarity 99.8%; Pred. No. 0; 3 Indels 0; Gaps 0; Matches 1676; Conservative 0; Mismatches 3; Indels 0; 0; Qy 30 CCCGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGAGGGCCCTGAAGGTCT 89 Line Indels Indels Indels 11 Indels 12 Db 268 CCAGGCAAGCAATGAGAATAGCACAGGACCTGAGAATGGGCCCGAGGGCCTTTG 149 Db 328 CCTACATCCCCGATGAGAATAGCACAGGGCCTGAGAATGGGCCCGAGGGCCTTTG 387	QY 150 GCTCTCGGGGTCAGCCCCAGGGGCTCACCTGTGGCAGCGGGGGCCCCAGCCAG	Db 568 ATAGGAAGGAACGCAGGTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGG 627 Oy 390 GCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGGGCTAAGGACACA 449 Db 628 GCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGCTAAGGACACCA 687 Oy 450 AAACGGCTGACGAGGTTCCCCTGAAGATCTTGGAGATAACTTTGTAGGGCTCTCA 509 Db 688 AAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCTCTCA 747 Oy 510 TTGGCAAGGAAGGACGGAAACTGAAGAAGAGAGAAAAATCACCA 569 Db 748 TTGGCAAGGAAGGAAGGAACTTAACAAGAAGAAAAAAAAA	QY 630 CCATCGAGAATTGTTGCAGGGCCGAGAAATAATGAAGAAAGTTCGGGAGGCCTATG 689 Db 868 CCATCGAGAATTGTTGCAGGGCGAGGAATAATGAAGAAGTTCGGGAGGCCTATG 927 QY 690 AGAATGATGTGGCCATGAGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGCTGTAG 749 Db 928 AGAATGATGTGGCCATGAGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGTAG 987 QY 750 GTCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCCCCCCAGCAGCGTTACTGGGGCTG 809

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BD209926 15-JUL-2003 1946 bp DNA linear PAT 17-JUL-2003 Isolated nucleic acid molecules encoding cancer-associated antigens, these antigens and method of using the same.

BD209226.1 GI:33019696 JP SO05212049-A/5.

Homo sapiens (human)
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1 (bases 1 to 1946)
Chen, Y.T., Gure, A., Tsang, S., Stockert, E., Jager, E., Knuth, A. and old, L.J.
Isolated nucleic acid molecules encoding cancer-associated
    1108 CCCAGGCAGTGGGCGCCATCATCGGCAAGAAGGGGCACATCAAACAACAGCTCTCCCGGT
                                                                                           TTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGG
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                                                             Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof Patent: US 67,6756-A 10-UN-2003; Location/Qualifiers
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and Old,L.J.
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Pred. No. 0;
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antigens, these antigens and method of using the same
Patent: JP 2002512049-A 5 23-APR-2002;
LUDMIG INSTITUTE FOR CANCER RESEARCH
OS Homo sapiens (human)
PN JP 2002512049-A/5
PD 33-APR-2002
PF 16-MAR-1999 JP 2000545030
PR 17-APR-1999 US 09/061709
PI YAO TSENG CHEN, ALI GURE, SOLAM TSANG, ELISABETH STOCKERT, ELKE
PI JAGER,
PI ALEXANDER KNUTH, LLOYD J OLD
PC C12N15/09, A61K35/12, A61K39/00, A61K39/39, A61P35/00, C07K16/32, PC C12N1/15,
PC C12N1/15,
PC C12N1/15,
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n=not determined(1622,1702,1771,1809,1833)
Key
Location/Qualifiers
1..1946
/organism='Homo sapiens (human)'.
Location/Qualifiers
1..1946
/organism='Homo sapiens"
/organism='Homo sapiens'
/organism='Homo
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PDEHMAMKALETPSGKVELGCKRIEIEHSVPKKGRSKIOIRNIPPOLEKWEVLDSILA
OYGTVENCEONVTESTEREDINGALMKLINGHOLENHALKVSYIPDEQIA
OGPENGREGGFGSRGOPAGNAPAKONOYYSNREDITALLVPTOYYGAIINTENTY
RNITKQTGSKIDVHRKENAGAAEKAISVHSTREGGSSACKMILEINHKEAKDTKTADE
NUCKARGOEINKKVNENAGAAEKAISVHSCOPTITISSLGOPILINNESAKITIVKGAIE
NCCRAEGOEINKKVNENAGAAEKAISHLIPGLNIAAVGLFPASSSAVPPPPSSYTGAAYSFENGOEINKKVNENASTENGOFFILTSTIOSHLIPGLNIAAVGLFPASSSAVPPPPSSY
             AF117106 2130 bp mRNA linear PRI 26-JAN-1999
Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete
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TVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILAQVKQQHQK
GQSNQAQARRK"
                                                                                                                                                                                                                                                   Location/Qualifiers

(bases 1 to 2130)

Nieleen, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H.,
Wewer, U.M. and Nielsen, F.C.

Wewer, U.M. and Nielsen, F.C.

Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
L. 2130

/organism='Homo_sapiens"
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                                                                                         Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 2130)
Nielsen, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H.,
Wewer, U.M., and Nielsen; F.C.
A family of insulin-like growth factor II mRNA-binding proteins
Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
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Product="IGF-II mRNA-binding protein 1"
protein_id="AAD09826.1"
/db_xrefe="GI:4191608"
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Pred. No. 0;
0; Mismatches
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/db_xref="taxon:9606"
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ilarity 99.2%;
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VPLKTLAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDLLLYNPERTITVKGAN NCCRAEGEIMKKVREAYENDVAAMSLOSHLTPGLMLAAVGLFPASSSAVPPPPSSV AAPYSSFMQAPEGENVQVFIPAQAVGAIIGKKGGHIKQLSRFASASIKIAPPETPD VANVITAPEAAQFKAGRIYGKLKEENFRGFKEVKLETHIRVPASAAGRVIGKG TVANLQMLTAAEVVVPRDQTPDENDQVIVKIIGHFVASQMAGRKIRDILAQVKQGH GQSNQAQRRK" 95.5%; Score 1631.8; DB 9; Length 2381; CCGGGGGAGCCATCATGAACTGCACACACTGCCCTGAAGGTCT 89 CCGGGGGAGCCATCATGAAGCTGAATGCCACCAGTTGGAGAACCATGCCCTGAAGGTCT 75 CCTACATCCCCGATGAAGCTGAATGGCCACAGTTGGAGAACCATGCCTGAAGGTCT 75 CCTACATCCCCGATGAAGCAGGAATGGCCACAGTTGGAGAACATGGCCCTGAAGGTCT 75 CCTACATCCCCGATGAAGCACAGGGACCTGAAGAATGGGCCCCAGGGGGGCCTTTG 11	210 CANAGARGAGGACATCACCATCGAGGCCCACCACCACCACATATTC 319 210 CANAGARGAGGGCCACCATCCCAAAACACCCCCACTCCAAGATAGCCCCTCCACCCCCCGG 319 310 ATAGCAAGAGGGCCCACTCCACACACACACACACCCCCACCCCCCCC
Db 1724 CCCAGGCACGAGGAAGTGACCAGCCCTCCTTCGAGTCCAGGACAACGG 1783 9y 1404 GCAGAAATCGAGAGTGCTCTCCCGGCAGCCTGAGAATCAGGAATCCGGACAC 1463 1784 GCAGAAATCGAGAGTGTGCTTCCCCGGCAGGCTGAGAATCAGGAATCCGGACAC 1843 9y 1464 NTGGCAGAAATCGAGATGTGCTCTCCCCGGCAGCTGAGAATCGGGACAC 1843 1844 CTGGCCGGGCTGAGATTGCTCCCCTTTGATTGAAAAAAGTGTTCCAGTGAGAAA 1903 1524 CTGGCCGGGCTGTAGATTGCCCACTTGATTGAGAAAAATTCCAGTGAGAAA 1903 1524 CTGGCCGGGCTGTAGATTGCCCACTTGATTGAGAAAAAATTCCCTTCAGGGAA 1903 1524 CTGGCCGGGCTGTAGATTGCCCCCAACTGATTGAGAAAAAATTCCCTTCAGGGAA 1903 1524 CTCTGATCTCTCAGCCCCAACACCCCACCCAATTGGCCCAACACTGTTTGCCCCTCGGGG 1963 1524 CTCTGATCTCTCAGCCCCAAACACCCACCCAATTGGCCCAACACTGTTTAAAAAAAA	RESULT 6 AP19824 AP19824 AP19824 AP19924 AP199254 AP199254 AP199254 AP199254 AP199254 AP199254 AP199254 AP19926 AP199

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Homo sapiens (human)
JP 2002017375-A/3242
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
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   HELIX RESEARCH INSTITUTE
OS THOMO SADJENS (human)
PN 42 200201375-A/3242
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHI
PI SHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAWA, KEIICHI NAGAI,
PI TETSUJI OTSUKI, HISASHI KOGA
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.2%;
Matches 1405; Conservative
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2780 bp DNA linear PAT 18-SEP-2002
BD127811
BD127811 GI:23222756
JP 2002017375-A/3242.
HOMO sapiens (human)
HOMO sapiens (butheria) Primates; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2780)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3242 22-JAN-2002;
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15 (bases 1 to 2780)
16 Isogair. and Otauki.T.

Direct Submission
17 and Otauki.T.

Direct Submission
18 Submitted (22-MAR-2002) Takao Isogai, Helix Research Institute,
18 Submitted (22-MAR-2002) Takao Isogai, Helix Research Institute,
18 Genomics Laboratory; 1532-3 Yana, Kiszazu, Chiba 292-0812,
18 Chomwing Trade and Industry of 189-438-52-3975, Fax:81-438-52-3986)
18 Economy, Trade and Industry of Japan; CDNA full insert sequencing:
18 Research Association for Biotechnology; CDNA library construction:
18 Institute of Medical Science, University of Tokyo, Laboratory of
18 Genome Structure; Human Genome Center; CDNA 5'- & 3'-end one pass
18 Sequencing and clone selection: Helix Research Institute (supported
19 Japan Key Technology Center etc.).
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/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Mul type="mtRNA"
/ Alone="NT2RR3000789"
/ Cell line="NT2R"
/ Cell Lype="teratocarcinoma"
/ Clone="lib="NT2R5"
/ Clone lib="NT2R5"
/ NOTE="cloning vector: pME185F13-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                     GCACCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAG
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AK074915.1 GI:22760672
Aligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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                                                                                                          CCCGGGGGGCCATCATGAAGCTGAATGGCCACTTGGAAAACCATGCCCTGAAGGTCT
                                                                            Gaps
                                                                            33,
                                              Length 2224;
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                                            Score 1165; DB 6;
Pred. No. 1.8e-282;
0; Mismatches 260;
/mol_type="unassigned DNA"
                                              Query Match
Best Local Similarity 82.8%;
Matches 1411; Conservative
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                                                                                           GCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGT
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GGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATT
                                                                                                               GCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGGAACTTCTTTGGT
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                               GCACCACCCGAAACACTGCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAG
                                                                                                                                                                                       CCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGG
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Patent: US 6255055-A 1 03-JUL-2001;
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Unclassified.
1 (bases 1 to 2224)
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/function="putative c-myc mRNA binding protein"
/note="CRD-BP"
/note="CRD-BP"
/codon_start=1
/codon_start=1
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/produclt-"coding region determinant binding protein"
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PDEHWAMAALEFSESGKNELDGEHSVEKQPSKTQIRNI PPOLKMENDSLIA
QYGTVENCEQVNTESETAVNVTVSNREQTRQAIMKLNGHQLENHALKVSYIPDEQIT
QGPENGRRGGFGSRGQPRQGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATI
RNITKGTQSKIDVHRKENAGAPAEKALSVHFPEGGSSCKMILENHAKZARDTKTADE
VPLKILAHNNFVGRLIGKSGRNLKKVEQDTETKITISSLQDITLIXNPFRTITVKTADE
VPLKILAHNNFVGRLIGKSGRNLKKVEQDTETKITISSLQDITLIXNPFRTITVRGAIE
NCGRAEQEINKKVRRAYENDYAAMSLOGSHLIFGLNLAAVGLFPASSSSAVPPPPSSYTG
AAPVSSFRQAPEGENVQVFTPAQAVGAIIGKKGQHIKQLSRRAASIKIAPPETPDSK
VRMVVITGPPEAQFKAQGRIYGKLKENFFGPKEEVKLETHIRVPASAAGRVIGKGGK
TVNBLQNLTAABVVVPRDQTPDENDQVIVKIIGHFYASQWAQRKIRDLLAQVKQQHQK
GQSNLAQARRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wisconsin
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Doyle,G.A., Betz,N.A., Leeds,P.F., Fleisig,A.J., Prokipcak,R.D.
                                                                                                                                                                                                                                                                                                  4 (bases 1 to 2223)
Leeds,P., Kren,B.T., Boylan,J.M., Betz,N.A., Steer,C.J.,
Gruppuso,P.A. and Ross,J.
Developmental regulation of CRD-BP, an RNA-binding protein that
stabilizes c-myc mRNA in vitro
Oncogene 14 (11), 1279-1286 (1997)
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Ross, J., Prokipcak, R.D., Leeds, P., Doyle, G.A.R., Betz, N.A.
Fleisig, A.J.
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Pred. No. 7.2e-282;
0; Mismatches 254; Indels 34; (
ribosome translocation and 3' untranslated regions and ribosome translocation Mol. Cell. Biol. 14 (3), 2119-2128 (1994) 94158886
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Submitted (25-APR-1998) McArdle Laboratory, University of Madison, 1400 University Ave., Madison, WI 53706, USA
                                                                                                                                                   (bases 1 to 2223)
Prokipcak, R.D., Herrick, D.J. and Ross, J.
Purification and properties of a protein that C-terminal coding region of human c-myc mRNA Biol. Chem. 269 (12), 9261-9269 (1994)

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    organism="Mus musculus"

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/db_xref="taxon:10090"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
1 (bases 1 to 2223)
Bernstein, P.L., Herrick, D.J., Prokipcak, R.D. and Ross, J.
Control of c-myc mRNA half-life in vitro by a protein capable of binding to a coding region stability determinant
Genes Dev. 6 (4), 642-654 (1992)
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Herrick,D.J. and Ross,J.
The half-life of c-myc mRNA in growing and serum-stimulated cells:
                                                                                                                   GCAAACTAAAAGAAGAATTTCTTTGGTCCCAAGGAGGAAGTAAAGCTAGAGAACCCACA
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                                                                                      GCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACA
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753517.

Location/Qualifiers
                                                                                                                                                                                         Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu
Gunarzene, P.H., Gazcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Submitted (30-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                   둬
                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kenneth R. Boheler (National Institute
Aging, USA)
                                                                                                                      cDNA Library Preparation: Vulan Piao and Minoru Ko (National Institute on Aging, NIH: http://lgsun.grc.nia.nih.gov/cDNA/) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mrna"
/mol_type="mrna"
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/db_xref="CDD:smart00360"
877. .1086
/note="KH; Region: K homology RNA-binding domain"
/db_xref="CDD:smart00322"
1504. .1719
/hote="KH; Region: K homology RNA-binding domain"
/db_xref="KH; Region: K homology RNA-binding domain"
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295-.2028
                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library (Long)"
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/note="Vector: pSPORT1"
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Length

DB 10;

Score 1161.6;

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Pred. No. 1.3e-281;
0; Mismatches 264; Indels
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                                                                                                                                                                                                                           protein 1"
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Pred. No. 3.2e-269;
0; Mismatches 178; Indels
                                                                                                                                                                                                                              binding
                                      /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                     /codon_start=1
/product="b-actin_zipcode
/protein_id="AAO16210.1"
/db_xref="G1:27464838"
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/note="rZBP1"
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86.2%;
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Matches 1285; Conserv
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
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1 (bases 1 to 2105)

Eom,T., Antar,L.N., Singer,R.H. and Bassell,G.J.
Localization of a beta-actin messenger ribonucleoprotein complex with zipcode-binding protein modulates the density of dendritic filopodia and filopodial synapses
J. Neurosci. 23 (32), 10433-10444 (2003)
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Eom.T., Singer, R.H. and Bassell, G.J.
Direct Submission
Submitted (27-AUG-2002) Neuroscience, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                     AATGAGTGGGAATCCGGGACACNTGGGCCGGGCTGTAGATCAGGTTTGCCCACTTGATTG
GCAAACTAAAAGAAGAATTTCTTTGGTCCCAAGGAGGAAGTAAAGCTAGAGACCCACA
                                                                                   1769 TACGGGTTCCGGCTTCAGCAGCCGGCCGTGTCATCGGCAAAAGGCGGCAAAACGGTGAATG
                                                                                                                                                        AGTTGCAGAATTTGACGCCAGCTGAGGTAGTACCAAGAGACCAGACCCCTGATGAGA
                                                                                                                                                                                          AGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGG
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VPLKILAHNNFVGRLIGKEGRNLKKYEQDTETKITISSLQDLTLYNPERTITYKKSIE
NCOYARQETKKYZEAYENDYAMSLQSHLIPGLNLAAVGLFPASSINAVPPPSSSVSG
AROYSSEMPPEGETVHVFIP TAQAVGATIGKKGCHIKQLSRFSASSIKIAPPEPSSSVSG
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NNVITGPPEAQFEXQGRIYGKLKENFFGFKEBVKLETHIRVPASSAGKIKOHQKG
VBLCNLTAAEVVVPRDQTPDENEQVIVKIIGHFYASQMAQRKIRDILAQVKQQHQKG
                                                  2 (bases 1 to 2021)
Oleynikov, Y.S., Ross, A.F. and Singer, R.H.
Direct Submission
Submitted (24-SEP-1997) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 CCAGGCAAGCCATCATGAAGTTAAACGGGCACCAGCTGGAGAACCACGTGCTGAAAGTCT
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                                                                                                                                                                                                                                                        /gene="ZBP1"
129. .1859
/gene="ZBP1"
/function="binds a zipcode element in beta-actin 1
3'UTR and is involved in its localization"
/note="beta-actin mRNA zipcode-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nuclear localization signal; NLS'
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.larity 81.3%; Pred. No. 2.1e-219;
Conservative 0; Mismatches 242;
Mol. Cell. Biol. 17 (4), 2158-2165 (1997)
97220007
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/gene="ZBP1"
/note="encodes KH-domain #4"
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                                                                                                                                                           /organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="texon:9031"
/cell_type="fibroblast"
/dev_stage="embryo"
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/gene="ZBP1"
/note="encodes R
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                         GGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTA
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Gallus gallus
Bukaryota; Metanista; Craniata; Vertebrata; Euteleosto
Bukaryota; Meso, Chordata; Craniata; Vertebrata; Euteleosto
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 2021)
1 (bases 1 to 2021)
1 (Ross, A.F., Oleynikov, Y., Kislauskis, E.H., Taneja, K.L. and
Singer, R.H.
Characterization of a beta-actin mRNA zipcode-binding protein
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90 CCTACATCCCCGATGAGCAGATAGCA	150 GCTCTCGGGGTCAGCCCCGCCAGGGC	210 AGCAAGTGGACATCCCCTTCGGCTC 1	270 GCAAGGAGGGCCACCATCCGCAAC 	330 ATAGGAAGGAGAACGCAGGTGCAGTI 	390 GCTGCTCCTCCGCTTGTAAGATGATCATCGTGCTGCTGCTGCTGCTGCAAAATGATC	450 AAACGGCTGACGAGGTTCCCCTGAAG	510 TTGGCAAGGAAGGACGGAACCTGAAG 	570 TCTCCTCGTTGCAAGACCTTACCCTT	630 CCATCGAGAATTGTTGCAGGGCCGAG	690 AGAATGATGTGGCTGCCATGAGC	744 CIGIAGGICTITICCCAGCITCAICC 1243 CAGITGCCTCTICCTGCCTCTCCTCCTGCTCTCCTGCTCTCCTGCTAGCTTCTCCTGCTAGCTTCTTCCTGCTAGCTA	804 GGGCTGCTCCCTATAGCTCCTTTATC	864 TCCCGCCCAGGCAGTGGGCGCCATC	924 CCCGGTTTGCCAGCGCCTCCATCAAC	984 GTATGGTTATCATCACTGGACCGCC 	1044 GCAAACTCAAGGAGGAGAACTTCTTI 	1104 TACGTGTGCCAGCATCAGCAGCTGGC 1600 TCCGTGTCCCCGCCTCGGCTGCAGGC

ò	1164	1164 AGTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGAGACCAGACCAGACCAGATGAGA 1223
q	1660	1660 AGCTGCAGAACCTGACGGTGCAGAGGTGGTGCTTCCACGGGATCAGACCCCTGATGAGA 1719
δŏ	1224	1224 ACGACCAGGTCATGTGAAAATCATGGGACATTTCTATGCCAGTCAGGTGGCTCAACGGA 1283
qq	1720	1720 ATGAGCAGGTCATTGTGAAGATCATCGGGCACTTCTATGCCAGCCA
δy	1284	1284 AGAICCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGG 1343
Op	1780	1780 AAATCCGGGGACATCCTGGCCCCAGGTGAAGCAGCAGCACCAGAAGGGACAGAGGGCGCCAGG 1839
ζ	1344	CCCAGGCACGGAAGTGA 1363
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2: \cgn2_6/ptodata/1/pubpna/PCT_MBW_PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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			Description	Sequence 5, Appli	Sequence 7, Appli	Sequence 2082, Ap	Sequence 1, Appli	Sequence 327, App	Sequence 745, App	Seguence 347, App	Sequence 347, App	Sequence 347, App		Sequence 347, App		347.	
SUMMARIES			ei ei	US-09-899-651-5	US-09-899-651-7	US-10-062-674-2082	US-09-873-637-1	US-09-764-864-327	US-09-764-864-745	US-09-735-705-347	US-09-850-716A-347	US-09-897-778-347	US-10-007-700-347	US-10-117-982-347	US-10-117-982-478	US-10-313-986-347	US-10-313-986-478
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7-778-44 7-778-45 07-700-4 07-700-4 17-982-4	US-10-313-986-44 US-10-313-986-45 US-09-850-778-428 US-09-897-778-428 US-10-007-700-42	0-313-986-48 0-313-986-48 0-117-982-47 0-313-986-47 -899-651-4 -735-705-175 -954-456-715	09-850-716A-17 09-897-778-175 09-00-007-700-17 -10-117-982-17 -10-313-986-17	US-10-117 US-10-313 US-09-899- US-10-097 US-10-648
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ALIGNMENTS

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                                                                        APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elke
APPLICANT: Stockert, Elke
APPLICANT: Muth, Alexander
APPLICANT: Older, Elke
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/899,651
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
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99.7%; Score 1703; Di
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1708; Conservative 0; Mismatches
; Sequence 5, Application US/09899651; Patent No. US20020111470A1; GENERAL INFORMATION:
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	### RESULT 4 US-09-870-637-1 15 Sequence 1, Application US/09873637 15 Sequence 1. Application US/09873637 16 Patent No. US/020206615434 17 TILE OF INVENTION: THE C-NYC CODING REGION DETERMINANT-BINDING PROTEIN 17 TILE OF INVENTION: THE C-NYC CODING REGION DETERMINANT-BINDING PROTEIN 17 TILE OF INVENTION: THE C-NYC CODING REGION DETERMINANT-BINDING PROTEIN 17 CURRENT PILIAND DATE: 2011-06-04 18 CURRENT PILIAND DATE: 2010-06-04 19 CURRENT PILIAND DATE: 2010-06-04 19 SEQ ID NO. 12 10 SEQ ID NO. 15 10 SEQ ID NO. 05 10 SEQ ID NO. 06 10 SEQ ID NO. 06 11 SEQ ID NO. 07 11 SEQ ID NO. 06 12 CCCGGGGGGCCATCATCATCAGGCCACCAGGTCAGGGGCCTTGGGGGGCTTGGGGGGCTTGGGGGGCTTGGGGGG
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2
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Pred. No. 0;
3; Mismatches
                                                      Query Match
Best Local Similarity 98.7%;
Matches 1084; Conservative
; ORGANISM: Homo sapiens
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SOTWARE: Patentin Ver. 2.0
SEQ ID NO 745
IENGTH: 1129
TYPE: DNA
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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Sequence 347, Application Us/09850716A
GENERAL NO. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455015
CURRENT APPLICATION NUMBER: US/09/850,716A
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Best Local Similarity 66.2%; Pred. No. 6.9e-171;
Matches 858; Conservative 0; Mismatches 433; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 347, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
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Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
Henderson, Robert A.
MCNeill, Patricia D.
Panger, Neil
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Bangur, Chaitanya S.
Hosken, Nancy
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Fan, Liqun
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Š	517	GGAAGGACGGAACCTGAAGAAGGTAGAGATACCGAGACAAAAATCACCATCTCCTC 576
qq	882	agaagaaagaaarciraaaaaaarraagcaagacacacacacaaaarcacgararcrcc 941
λ	577	GTIGCAAGACCTTACCCTTACAACCCTGAGAGACCATCACTGTGAAAGGGGGCCCATCGA 636
qq	942	ATTGCAGGAATTGACGCTGTATAATCCAGAACGCACTATTACAGTTAAAGGCAATGTTGA 1001
'n	637	GAATTGTIGCAGGGCCGAGCAGGAATAATGAAGAAAGTICGGGAGGCCTATGAGAATGA 696
අු	1002	GACATGTGCCAAAGCTGAGGAGGAGATCATGAAAAATCAGGGAGTCTTATGAAAATGA 1061
λŏ	697	TGTGGCTGCCATGAGCTCTCACTGATCCTGGCCTGAACTGGCTGCTGTAGG 750
qq	1062	TATTGCTTCTATGAATCTTCAAGCACATTAATTCCTGGATTAATCTGAACGCCTTGGG 1121
δ	751	TCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTGC 810
qq	1122	TCTGTTCCCACCCACTTCAGGGATGCCACCTCCACCTCAGGGCCCCCTTCAGCCATGAC 1181
λ̈́o	811	TCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGC 870
qq	1182	TCTCCCCTACCCGCAGTTTGAGCAATCAGAAACGGAGACTGTTCATCTGTTTATCCCAGC 1241
δγ	871	CCAGGCAGTGGGCCATCATCGGCAAGAAGGGGCAGCACCATCAAACAGCTCTCCCGGTT 930
Db	1242	rctarcagroscreccarcarcascascascascascascarcascascarcascarcascarcascarcascascarcascascascascascascascascascascascascasc
δλ	931	TGCCAGGGCCTCCATCAAGATTGCACCACCGAAACACCTGACTCCAAAGTTCGTATGGT 990
DP	1302	TECTGGAGCTTCAATTAAGATTGCTCCAGGGAAGCACCAGATGCTAAAGTGAGGATGGT 1361
Š	166	TATCATCACTGGACCGCAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACT 1050
qq	1362	GATTATCACTGGACCACAGAGGCTCAGTTCAAGGCTCAGGAAGAATTTATGGAAAAAT 1421
λõ	1051	CAAGGAGGAGAACTICTITGGICCCAAGGAGGAAGTGAAGCTGGAGGACCCACATATOTTO
qq	1422	TAAAGAAGAAACTTTGTTAGTCCTAAAGAAGAGGTGAACTTGAAGCTCATATCAGAGT 1481
δy	1111	GCCAGCATCAGCAGCTGGCTGGGCAAAGGTGGAAAAACGGTGAACGAGTTGCA 1170
Db	1482	GCCATCCTTTGCTGCTGCTGCAGAGTTATTGGAAAAGGAGGCAAAAAGGGAGAAAAGGAGAAAAGGAGAAAAGGAGAAAAGGAGA
٥٨	1171	GAATITGACGCCAGCTGAGGTGCTACCAAGAGACCAGCCCCTGATGAGAACGACCA 1230
Db	1542	GAATTTGTCAAGTGCAGAAGTTGTTGTCCCTCGTGACCAACACCTGATGACAA 1601
ζλ	1231	GGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCG 1290
qq	1602	AGTGGTTGTCAAAATAACTGGTCACTTCTATGCTTGCCAGGTTGCCCAGAGAAAATTCA 1661
δλ	1291	AGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAG 1327
qa	1662	GGAAATTCTGACTCAGGTAAAGCAGCACCAACAG 1698

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           TGCCAGGGGCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGGT
                                                                               TATCATCACTGGACCGCCAGAGCCCCAATTCAAGGCTCAGGGAAGAATCTATGGGAAACT
                                                                                                            1602 AGTGGTTGTCAAAATAACTGGTCACTTCTATGCTTGCCAGGTTGCCCAGAAAAATTCA
                                                                                                                                                                                                                                   GCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAAGGTGGAAAAAACGGTGAACGAGTTGCA
                                                                                                                                                                                                                                                               1171 GAATTTGACGCAGCTGAGGTGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCA
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JAPPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.

JAPPLICANT: Fanger, Thomas S.

APPLICANT: Fanger, Thomas S.

APPLICANT: Carter, Darrick
JAPPLICANT: Watanabe, Yoshiniro
APPLICANT: Penderson, Robert A.

APPLICANT: Fanger, Neil
JITLE BY INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
JITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
JITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEG ID NOS: 467

SOPTWARE: FastSEQ for Windows Version 4.0
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66.2%; Pred. No. 6.9e-171;
ive 0; Mismatches 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 347, Application US/09897778; Patent No. US20020147143A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 858; Conserv
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US-09-897-778-347
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                                                                                                                                                                                                                                                                                                                      CCCCGATGAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGGGCTTTGGCTCTCG 156
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                                                                                                                                                                      Score 582.2; DB 9;
Pred. No. 6.9e-171;
0; Mismatches 433;
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFIWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347
                                                                                                                                                                        34.1%;
                                                                                                                                                                  Query Match
Best Local Similarity 66.2°
Matches 858; Conservative
                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-850-716A-347
                                                                             LENGTH: 1740
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                                                                                                                    US-10-007-700-347, Application US/10007700

Publication No. US20030064947A1

FUNDALICANT: NO. US20030064947A1

FUNDALICANT: Wang, Yajun

FAPPLICANT: Wang, Ajun

FAPPLICANT: Kalos, Michael D.

APPLICANT: Kalos, Michael D.

FAPPLICANT: Retier, Marc W.

APPLICANT: Retier, Marc W.

APPLICANT: Retier, Marc W.

APPLICANT: Retier, Marc W.

APPLICANT: Panger, Thomas S.

APPLICANT: Panger, Towarink

APPLICANT: Penger, Yoshinro

APPLICANT: Penger, Yoshinro

APPLICANT: Penger, Yoshinro

APPLICANT: Peckman, David W.

APPLICANT: Peckman, David W.

APPLICANT: Poy, Teres M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE FILE SPERENCE: 210121.455017

CURRENT APPLICATION NUMBER: US/10/007,700

CURRENT PILNG OF THE SACESQ FOR WINDER: DAVIS SOFTWARE: FALSE FARESE FASTESQ FOR WINDER: 2001-11-30

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FASTESQ FOR WINDOW: 1 TANGER.

TENCH DAVIS SACESO FOR WINDOW: 1 TENCH DAVIS
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larity 66.2%; Pred. No. 6.9e-171
Conservative 0; Mismatches 433
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ORGANISM: Homo sapiens
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APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT PAPLICATION NUMBER: US/10/117,982
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 484
SOFTMARE: RESESEQ FOR Windows Version 4.0
LENGTH: 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 582.2; DB 15;
Pred. No. 6.9e-171;
0; Mismatches 433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.2'
Matches 858; Conservative
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-10-117-982-347
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Sequence 347, Application US/10117982
Publication No. US20030138438A1
GENERAL INFORMATION
APPLICANT: FOY, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Handerson, Yoshinhro
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Spies, Gregory A.
APPLICANT: Spies, Gregory A.
APPLICANT: Fan, Liqun

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942 ATTGCAGGAATTGACGCTGTATAATCCAGAACGCACTATTACAGTTAAAGGCAATGTTGA 1001
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Publication No. US20030138438A1
GENERAL INFORMATION:
APPLICANT: Fory, Teresa M.
APPLICANT: Proy, Teresa M.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Manabe, Yoshihiro
APPLICANT: Mericle, Barbara
APPLICANT: Mericle, Barbara
APPLICANT: Fan, Liqun
APPLICANT: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF CURRENT FLLING DATE: 2002-04-05
CURRENT FLLING DATE: 2002-04-05
NUMBER OF SECIED NOS: 484
LIGHTH: LIGHTH: LIGHTH AND ATRA
LIGHTH: LIGHTH APPLICATION 478
LIGHTH APPLICATION
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Pred. No. 6.9e-171;
0; Mismatches 433;
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Best Local Similarity 66.2%;
Matches 858; Conservative
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GITIGCAAGACCITTACCATCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGA
                                                                 GAATTGTTGCAGGCCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCCCTATGAGAATGA
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US-10-313-986-478

US-10-313-986-478

Squence 479, Application US/10313986

Publication No. US20030236209A1

GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.

APPLICANT: Matanabe, Andria

APPLICANT: Reed, Steven G.

APPLICANT: Read, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121-455C19

CURRENT APPLICATION NUMBER: US/10/313,986

CURRENT APPLICATION DIAGNOSIS OF LUNG CANCER

NUMBER OF SEQ ID NOS: 560

SSCTWARE: FastSEQ for Windows Version 4.0

TYPE: DNA
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Pred. No. 6.9e-171;
0; Mismatches 433;
                                                                                    AGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAG
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cal Similarity 66.2%;
858; Conservative
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; ORGANISM: Homo sapiens
US-10-313-986-347
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US-10-313-986-347
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   GATTATCACTGGACCACCAGAGGCTCAGTTCAAGGCTCAGGGAAGAATTTATGGAAAAAT 1421
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                                                                       TAAAGAAGAAACTTTGTTAGTCCTAAAGAAGAGGTGAAACTTGAAGCTCATATCAGAGT
                                                                                                                                             GAATTTGACGCCAGCTGAGGTGCTACTACCAAGAGACCAGACCCCTGATGAGAACGACCA
                                       CAAGGAGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGT
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APPLICANT: Mang, Tongtong
APPLICANT: Mannerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
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Pred. No. 6.9e-171;
0; Mismatches 433;
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Patent No. US20020147143A1
GENERAL INFORMATION:
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66.2%;
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Matches 858; Conservative
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ORGANISM: Homo sapiens
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                                                                                        Gaps
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                                                      DB 16; Length 1740;
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                                                    Score 582.2; DB 16;
Pred. No. 6.9e-171;
0; Mismatches 433;
                                                   34.18;
                                               Query Match
Best Local Similarity 66.2<sup>3</sup>
Matches 858; Conservative
; ORGANISM: Homo sapiens
US-10-313-986-478
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Search completed: July 13, 2004, 23:41:03 Job time : 798 secs

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GenCore version 5.1.6
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July 13, 2004, 14:50:27 ; Search time 699 Seconds (without alignments) 10380.433 Million cell updates/sec Run on:

US-09-270-437D-5

1708 1 agggacgctgccgcaccgcc.....atttccttcaggttttaaaa 1708 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Scoring table:

6747726 Total number of hits satisfying chosen parameters: 3373863 segs, 2124099041 residues Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:* 1: qeneseqn1980s:* geneseqn1980s:* Database :

geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2000s:* geneseqn2001as:* geneseqn2003bs:*geneseqn2003cs:* geneseqn1990s:* geneseqn2004s: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaz36151 DNA encod	An	N	~	Aas26148 Human cDN	Abx73489 Human nov	Human	Abx73907 Human nov	Aak91969 Human cDN		Aac66035 Human lun	Abl49254 Human lun	Abg92440 Human lun	9 Human	Human	Abq92483 Human lun		Ada28540 Recombina	Ada28537 Recombina	Abl49283 Human lun	Abq92469 Human lun	Ada28518 Recombina	Ada28437 Human lun
	1	AAZ36151	AAZ36153	AAK94782	AAZ10617	AAS26148	ABX73489	AAS26566	ABX73907	AAK91969	AAK93655	AAC66035	ABL49254	ABQ92440	ABL49299	ABL49297	ABQ92483	ABQ92485	ADA28540	ADA28537	ABL49283	ABQ92469	ADA28518	ADA28437
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o l to	Query	99.7	97.7	81.3	68.0	63.5	63.5	62.6	62.6	42.9	42.9	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34,1	34.1	34.1	34.1	34.1	34.0
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Aaz36150 DNA encod Aac65900 Human lun Abl65405 Lung canc Abl49119 Human lun	Human Human Human Human	Action Factor Adagement Con Aba9958 Human KOC Aba876779 DNA encod Aba886150 DNA encod	4 8 2 7 1 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		Aca90176 cDNA enco Aas26153 Human cDN Abx73494 Human nov
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ALIGNMENTS

RESULT 1

Knuth A, Cancer associated antigen; KOC-2; cancer; vaccine; CT7; ss. Jager E, DNA encoding cancer associated antigen KOC-2. Stockert E, AAZ36151 standard; DNA; 1708 BP. (LUDW-) LUDWIG INST CANCER RES. 98US-00061709. 99WO-US005766. Gure A, Tsang S, (first entry) W09954738-A1. Homo sapiens. 16-MAR-1999; 17-APR-1998; 11-FEB-2000 28-OCT-1999. AAZ36151; chen Y, AAZ3615:

develop Nucleotides representing cancer-associated genes, used to develo products for the diagnosis, monitoring and treatment of cancers.

WPI; 2000-013284/01.

old LJ;

Claim 55; Page 40; 44pp; English.

The present sequence represents a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CTC-1. The CT7 polymocleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and lucine, and an almost invariable core of the peptide given in AAY4837. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic I cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony

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Best Local Similarity 100.0%; Pred. No. 0;
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genes, used to develo treatment of cancers.

Nucleotides representing cancer-associated products for the diagnosis, monitoring and Claim 55; Page 42; 44pp; English LUDWIG INST CANCER RES WPI; 2000-013284/01. Gure A, Chen Y,

The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 plotyluciotide was isolated from SK-WEL-37 melanoma cells. The CT7 polynuciotide was some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats fich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAY43877. The CT7 polypeptide can be processed to peptides which provoke lysis by evtolytic T cells. The polynuciectides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF)

Sequence 1946 BP; 502 A; 528 C; 553 G; 358 T; 0 U; 5 Other;

327 149 209 269 329 449 569 387 447 507 567 389 627 687 509 747 629 867 807 83 CCTACATCCCCGATGAGGAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGGGGCTTTG GCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAGAGGCTAAAGGACACCA CCCGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAACCATGCCTGAAGGTCT AGCAAGTGGACATCCCCCTTCGGCTCCTGGTGCCCACCAGTATGTGGGGTGCCATTATTG AGCAAGTGGACATCCCCTTCGGCTCCTGGTGCCCACCCAGTATGTGGGGTGCCATTTG 508 GCAAGGAGGGGCCACCATCCGCAACATCACAAACAGACCCAGTCCAAGATAGACGTGC AAACGGCTGACGAGGTTCCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCA TTGGCAAGGAAGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAATCACCA 748 TIGGCAAGGAAGGAACCIGAAGAAGGIAGAGCAAGAIACCGAGACAAAAAICACCA ccadecaadccarcardaagcrdaareeccaccagrregagaaccareccrgaaggrcr CCTACATCCCCGATGAGCAGATAGCACAGGACCTGAGAATGGGCGCCGAGGGGGCTTTG GCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCCAGCCAAGCAGC GCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGC ATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGG GCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCA AAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCA TCTCCTCGTTGCAAGACCTTACCACCTTGAGAGGACCATCACTGTGAAGGGGG Gaps DB 3; Length 1946; . 0 3; Indels Score 1669.2; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 99.8%;
Matches 1676; Conservative C 448 390 688 30 268 328 150 388 210 270 330 568 450 510 90 628 570 δ OC ò D D à g ਨੇ ద õ qq ò a ò qq ò 셤 ò 음 ծ

1049 1109 1409 1047 1167 1227 1287 TCAAGGAGGAGAAACTICTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCCACATACGTG 1347 1407 1229 1467 1289 1527 1587 1469 1707 1767 1589 803 CICCCIATAGCTCCTTTATGCAGGCTCCCGAGGAGGATGGTGCAGGTGTTATCCCCG GAGACATCCTGGCCCAGGTTAAGCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGG CCATCGAGAATTGTTGCAGGGCCGAGGAAATAATGAAGAAAGTTCGGGGAGGCCTATG AGAATGATGTGCCTGCCATGAGCTCTCACCTGATCCTGGACCTGAACCTGGCTGCTGTAG 988 GICTITICCCAGCTICATCCAGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTG CCCAGGCACCATCATCGGCAAGGAGGGGCAGCACATCAAACAGCTCTCCCGGT TIGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGG TTATCATCACTGGACCGCCAGAGGCCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAAC 1228 TTATCATCATCACTGGACCGCCAGAGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAAC TGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAAAGGGTGAAAAACGGTGAACGGTTGC AGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCC CACGAGGAAGTGACCAGCCCCTCCCTGTCCTTNGAGTCCAGGACAACAACAACGGGCAGAA AGAATGATGTGGCTGCCATGAGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGCTGTAG GTCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTG CTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGGATGGTGCAGGTGTTTATCCCCG TCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCCACATACGTG 1170 AGAATTTGACGGCAGCTGAGGTGGTACCAAGAGACCAGACCCCTGATGAGAACGACC AGAATTTGACGGCAGCTGAGGTGGTACCAAGAGACCAGACCCCTGATGAGAACGACC GAGACATCCTGGCCCAGGTTAAGCAGCACCATCAGAAGGGACAGAGTAACCAGGCCCAGG CACGGAGGAAGTGACCAGCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACGGGCAGAA ATCGAGAGTGTGTCTCCCCGGCAGGCCTGAGAATGAGTGGGAATCCGGGACACACNTGGGC ATCGAGAGTGTGCTCTCCCCGGCAGGCCTGAGAATGAGTGGGAATCCGGGACACACNTGGGC CGGGCTGTAGATCAGGTTTGCCCCACTTGATTGAGAAGATGTTCCAGTGAGGAACCCTGA casacrarasarcasarrasacarrasarrasasararrasarsarsasasarcarsa TOTINTCAGCCCCAAACACCCCACCCAATTGGCCCCAACACTGTNTGCCCCTCGGGGTGTCAG reinteagceceaaacaceceaecearregeceaacacacreintgeceeregggerereag AAATINTAGCGCAAGGCACTITTAAACGTGGATTGTTTAAAGAAGCTCTCCAGGCCCCAC CCCAGGCAGTGGGCGCCATCATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGT TTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGG TGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAAGGTGGAAAAACGGTGAACGAGTTGC 1230 AGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCC 810 1110 1348 1048 1168 1050 1288 1410 868 069 928 870 1108 930 990 1408 1468 1290 1528 1350 1588 1648 1470 1708 1530 1768 1590 1828 1650 1888 750 임 셤 ð g ò g ò à qq ઠે ద ò 음 ∂ 장 역 ò d 8 g ò d à ď ò q ò 셤 g $\dot{\delta}$ ò

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                                                                         AACCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length cDNA ere obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length muman cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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                                                                                                                                                                                                                                              full length cDNA; cDNA synthesis; oligo-capping; ss.
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Pred. No. 0;
0; Mismatches
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99.2%;
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Best Local Similarity 82.7%;
Matches 1409; Conservative
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P-PSDB; AAY30649.
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   CCCAGGCACGGAGGAAGTGA-CCAGCCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACG 1402
                                                                                                                                 AGAACAATGITCCAGIGAATCCIGAICTCTCGCCCCCAA--TIGAGCCAGCIGCCA 2081
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                                                    cccaedcacedadadadaccccccccccrcrercarrecricaadarcaeda 1904
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                                                                                                                   AATGAGTGGGAATCCGGGACACNTGGGCCGGGCTGTAGATCAGGTTTGCCCCACTTGATTG 1501
                                                                                                                                                           CAACACTGTNTGCCCCTCGGGGTGTCAGAATTNTAGCGCAAGGCACTTTTAAACGTGGA 1621
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                                                                                                                                                                                                                                             TTGTTTAAAGAAGCTCTCCAGGCCCCACCAAGAGGGTGGATCACACCTCAGTGGGAAGAA 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; order; oerebrovascular disorder; Alzheimer; angiogenesis; nervous system disorder; Alzheimer; disease; infection; ocular disorder; conneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                         ------ATCGAGAGTGTGCTCTCCCCGGCAGGCCTGAG
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44-FEB-2000; 2000US-0186628P.

24-FEB-2000; 2000US-0186464P.

02-MAR-2000; 2000US-0186350P.

17-MAR-2000; 2000US-0199076P.

18-APR-2000; 2000US-0199123P.

19-MAR-2000; 2000US-0199123P.

19-MAR-2000; 2000US-020515P.

07-JUN-2000; 2000US-020515P.

08-JUN-2000; 2000US-0214886P.

08-JUN-2000; 2000US-0214886P.

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diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. arreadisc arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Arbieimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to respent te tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAATGAAGAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCCATGAGC-----TC 714
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Pred. No. 3.9e-297;
0; Mismatches 6; Indels 6:
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Best Local Similarity 98.9%;
Matches 1102; Conservative
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                                       ATTGGCCCAACACTGTCTGCCCCTCGGGGTGTCAGAAATTCTAGCGCAAGGCACTTTTAA
                                                                                                                                                                                       1038 ACGTGGATTGTTTAAAGAAGCTCTCCAGGCCCCACCAAGAGGGTGGATCACTCAGTG
                       GCCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGGCTGTAGATCAGGTTTGCCCAC
                                                                                              918 TIGATIGAGAAGAIGITCCAGIGAGGAACCCIGAICTCTCAGCCCCAAACACCCCA
                                                                                                                       1555 ATTGGCCCAACACTGTNTGCCCCTCGGGGTGTCAGAAATTNTAGCGCAAGGCACTTTTAA
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2000US-0218290P.
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14-AUG-2000; 2
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07-JUL-2000; 2
07-JUL-2000; 2
11-JUL-2000; 2
11-JUL-2000; 2
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The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatodia arthritis and multiple solerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atheroscierosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 CCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGA
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98.9%; Pred. No. 3.9e-297;
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                           2000US-0229513P.
2000US-0231413P.
2000US-0234223P.
2000US-0234274P.
2000US-0234997P.
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2000US-0236327P.
2000US-0236367P.
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2000US-0237037P.
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P-PSDB; ABU55229.
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RUBEN S M.
BARASH S C.
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01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
08-SEP-2000;
21-SEP-2000;
21-SEP-2000;
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02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
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661 AATAATGAAGAAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCCATGAGC----TC

18 CGCTGAGAGGACCATCACTGTGAAGGGGCCCATCGAGAATTGTTGCAGGCCGAGGA

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(first entry)

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                                                    AGTCCCGCCGCCCTCCCAGCAGCGTTACTGGGGCTGCTCCTATAGCTCCTTTATGCAGGC
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TCACCTGATCCCTGGCCTGAACCTGGCTGCTGTAGGTCTTTTCCCCAGCTTCATCCAGCGC
             TCACCTGATCCCTGGCCTGAACCTGGCTGTAGGTCTTTTCCCAGCTTCATCCAGGC
                                                                                                          TCCCGAGCAGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCATCATCGG
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RESULT 7 AAS26566 ID AAS26566 standard; cDNA; 1129

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Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; optalmalodical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer; disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                               Seq ID 745.
                                                                                                    Human cDNA encoding a novel secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2000; 2000US-0179065P.
04-FEB-2000; 2000US-018636P.
02-MAR-2000; 2000US-0186360F.
02-MAR-2000; 2000US-0186360F.
16-MAR-2000; 2000US-0186360F.
16-MAR-2000; 2000US-0198134P.
17-MAR-2000; 2000US-0198134P.
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30-JUN-2000; 2000US-02148868.
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14-AUG-2000; 2000US-0225266P.
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14-AUG-2000; 2000US-0225275P.
14-AUG-2000; 2000US-0225279P.
14-AUG-2000; 2000US-0225279P.
14-AUG-2000; 2000US-0225279P.
14-AUG-2000; 2000US-0225344P.
01-SEP-2000; 2000US-0229344P.
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08-NOV-2000; 2000US-0246524P.
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08-NOV-2000; 2000US-0246528P.
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26-SEP-2000;
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to concition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a leavisting symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (EBLSA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiocors cather disorders e.g. cardiocors and interval and contain disorders e.g. cardiocors cather disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. conneal infection. Cor summy other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to respentate tissues and in chemotaxis. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, cor respentate tissues and in chemotaxis. The polypeptides can also be used compensately tissues, to capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present compensate content of the printed sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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                   17-NOV-2000, 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
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05-JAN-2001; 2001US-0259678P
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CTGAACCTGCTGTTGTTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCCCCCC

CTGAACCTGGCTGCTGTAGGTCTTTTCCCAGCTTCATCCAGGGCAGTCCCGCCGCCTCCC

CGGGAGGCCTATGAGAATGATGTGGCTGCCATGAGCCTGCAGTCTCACCTGATCCCTGGC

CGGGAGGCCTATGAGAATGATGTGCTGCCATGAGC-----TCTCACCTGATCCCTGGC

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181 AGCAGCGTTACTGGGGCTGCTCCTTTATACTGCAGGCTCCCGAGGAGATG

791 AGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATG

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disorder;
muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
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04-FEB-2000; 2000US-011686P.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                                                                                                                                             The invention relates to human novel polypeptides and their associated polymuclectides. The polypeptides and polymuclectides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. gastrointestinal disorders, pulmonary disorders, reproductive disorders, gastrointestinal disorders, pherein's anomaly and hypoplastic left (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial human control diseases). Sequences ABX73173-ABX74167 represent
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                              New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1129 BP; 318 A; 296 C; 302 G; 210 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ed. No. 1e-292;
Mismatches 5; Indels
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                                                                                                                                          781 AGGACAACGAGGCAGAAATCGAGAGTGTGCTCCCCGGCAGGCCTGAGAATGAGTGG 840
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                                                              1271 ATGGCTCAACGGAAGATCCGAGACATCCTGGCCCCAGGTTAAGCAGCAGCATCAGAAGGG
                                                                                         AGGACAACAACGGGCAGAAATCGAGAGTGTGCTCTCCCCGGCAGGCCTGAGAATGAGTGG
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                               661 Aredericaaceaacareceagacarecredeceagerraageageageareageaageaa
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K, Kojima S, Otsuki T, Koga
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and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a CDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EDO
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                                                                                                                                                                                                         Length 833;
                                                                                                                                                                             Sequence 833 BP; 223 A; 225 C; 215 G; 166 T; 0 U; 4 Other;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                        Score 732.8; DB 4;
Pred. No. 3.6e-197;
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Matches 802; Conservative
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3' -ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA essily whithout any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
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                                                                                                                                                                                                                                                                                                                                                 Koga
                                                                                                                                                                                                                                                                                                                                                                                                     full length cDNA clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 11; SEQ ID NO 2115; 1380pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 833;
                                                                                                                                                                                                                                                                                                                                     hii S, Kawai
Otsuki T, Ko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 215 G; 166 T; 0 U; 4 Other;
                                                                                                                    Human; full length cDNA; cDNA synthesis; oligo-capping; ss
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                                                                                                                                                                                                                                                                                                                                     Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 732.8; DB 4;
Pred. No. 3.6e-197;
0; Mismatches 14;
                                                                                         cDNA clone representative sequence, SEQ ID
                                                                                                                                                                                                                                                                                                                                     Hayashi K, Isl
K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                      synthesizing
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a T, Nagai
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2000JP-00118774.
2000JP-00183765.
            CDNA; 833
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Best Local Similarity 96.9%;
Matches 802; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 833 BP; 223 A; 225
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genetic manipulation.
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            AAK93655 standard;
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02-MAY-2000;
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                                                                                                                                                                                                                                                                 This invention describes a novel isolated polypeptide (I) which comprising an imminogenic portion of a lung tumour protein or variant (P2) which have cytostatic activity. The polypeptides and polymorlectides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polymuclectides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCACTAGACAAACTGAATGGATTTCAGTTAGAGAATTTCACCTTGAAAGTAGCCTATAT 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 582.2; DB 3; Length 1740; Pred. No. 2.8e-154; 0; Mismatches 433; Indels 6;
                                                                    Isolated polypeptide comprising an immunogenic portion of a protein is used for detecting and monitoring progression of in a patient,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 U; 0 Other;
                                                                                                                                                                                                        Page 258-259; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.2%;
Matches 858; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development of cancer
                                                                                                                                                                                                        Claim 1a;
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                                                                                                                                                                                  AACCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABJ48959 to ABJ49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adababarcecececrecres da basa de la contracta 
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      Henderson R.
Fanger GR;
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SX, Kalos MD,
, Marnerakis M,
!, Peckham DW;
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Pred. No. 2.8e-154;
0; Mismatches 433;
Skeiky YAW, Li SX,
pr N, Retter MW, N
pr D, Watanabe Y,
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Best Local Similarity 66.2%;
Matches 858; Conservative
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                                                    TCTTTTCCCAGCGTTCATCCAGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTGC
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Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine; gene;
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Durham M, Fanger GR, Vedvick TS;
                                                                       ID NO:347.
                                                                      associated cDNA sequence SEQ
                                                                                                                                                                                                                                        A, Skeiky YAW, Li S
Fanger N, Retter MW,
                  BP.
                 ABQ92440 standard; cDNA; 1740
                                                                                                                                                                                     12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
                                                                                                                                                                    30-NOV-2001; 2001WO-US047576.
                                                    (first entry)
                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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                                                                      Human lung
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942 ATTGCAGGAATTGACGCTGTATAATCCAGAACGCACTATTACAGTTAAAGGCAATGTTGA 1001

882 AGAAGGAAGAATCTTAAAAAATTGAGCAAGACACAGACACTAAAATCACGATATCTCC 577 GTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGGCCATCGA

GGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCCTC

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TGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAA 822 AGAAGAGATCCCCTTGAAGATTTTAGCTCATAATAACTTTGTTGGACGTCTTATTGGTAA

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The present invention describes isolated human lung carcinoma polymucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polymucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and desermining the presence of a cancer in contacting the amount of polymucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and desermining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ22146 and ABBPE1866 to increase.
                                                                                                   Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
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    Foy
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Pred. No. 2.8e-154;
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  Peckham
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Local Similarity 66.2%;
les 858; Conservative (
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                                      WPI; 2002-583465/62.
P-PSDB; ABP61917.
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Carter D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
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Fanger GR;
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Pred. No. 2.8e-154;
0; Mismatches 433; Indels
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Retter MW, Marnerakis M,
Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                  polypeptides,
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lung cancer or stimulating an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 370; 374pp; English.
                                                                                                                                                                                                    Wang A, Skeiky YAW,
PD, Fanger N, Retter
TS, Carter D, Watanab
2000US-00643597.
2000US-00662786.
2000US-00685696.
2000US-00735705.
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Best Local Similarity 66.29
Marches 858; Conservative
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                                                                                                                                                         (CORI-) CORIXA CORP.
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P-PSDB; ABB75054
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The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynuclectides, antibodies, proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. AB48959 to AB49300 and AB74946 to ABB75070 represent sequences used in the exemplification of the present

Sequence 1743 BP; 527 A; 406 C; 418 G; 392 T; 0 U; 0 Other;

treating

useful for

Polynucleotides encoding lung tumor polypeptides, lung cancer or stimulating an immune response.

Claim 1; Page 367; 374pp; English.

RA;

/ YAW, Li SX, Kalos MD, Retter MW, Marnerakis M, Watanabe Y, Peckham DW;

Skeiky YAW,

Wang A,

(CORI-) CORIXA CORP

PD, Fanger N, TS, Carter D,

PD,

Vedvick

2002-090513/12

P-PSDB; ABB75053

2000US-00630940. 2000US-00643597. 2000US-00662786. 2000US-00685696. 2000US-00735705.

02-AUG-2000; 2 21-AUG-2000; 2 15-SEP-2000; 2 09-OCT-2000; 2 12-DEC-2000; 2

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AGCACTAGACAACTGAATGGATTTCAGTTAGAGAATTTCACCTTGAAAGTAGCCTATAT
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    Score 582.2; DB 6; Length 1743;
Pred. No. 2.8e-154;
0; Mismatches 433; Indels 6;
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    34.1%;
llarity 66.2%;
Conservative
Query Match
Best Local Similarity
Matches 858; Conserv
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Human lung tumour L523S recombinant polynucleotide SEQ ID NO:447

immune response; ss

Human; lung

WO200200174-A2

Homo

(first entry)

28-JUN-2001; 2001WO-US021065.

ABL49297 standard; cDNA; 1743

ABL49297

641

396 761 456

516 821

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GCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAAGGTGGAAAAACGGTGAACGAGTTGCA 1170
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              942 ATTGCAGGAATTGACGCTGTATAATCCAGAACGCACTATTACAGTTAAAGGCAATGTTGA 1001
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577 GTIGGAAGACCTIACCCTITACAACCCTGAGAGGACCAICACTGTGAAGGGGGCCAICGA
                                                GAATTGTTGCAGGCCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCCTATGAGAATGA
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J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Huizar, L. Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.. Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Lusy, D.; Sakano, H. Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Fraser, C.M.; Venter, J.C.; Davis, R.W. alysis of chromosome 1 of the plant Arabidopsis. 1075 1455 AAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGC 1125 ----- 1219 SACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGC 1275 ATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAG 1335 2AGGCACGGAGGAAGTGACCAGCCCCTCCCTGTCCCTTNGAGTCCAGGAC 1395 3GGCCGGCCTGTAGATCAGGTTTGCCCACTTGATTGAGAAGATGTTCCA 1515 TIGATICTINTICAGCCCCAAACACCCCACCCAATTIGGCCCAACACTGTINTIGCC 1575 3luAspAsnAlaThrIleAsnSerSerAspAlaIleGluLlysProLy 659 GluargMetValThrileAsnGlyAspAspLeuGlnLeuLeuLysAlaGl 679 SerHisMetLeuArglleArgThrGluValSerValProThrArglleIl 719 843 C24.19 [imported] - Arabidopsis thaliana haliana (mouse-ear cress) uence_revision 02-Mar-2001 #text_change 31-Mar-2001 ::: |||::: ||| PheSerLysIleAlaGluThrSerSerSerLeuProSerSerGlyMetAs :::||| |IleProGluGluGluArgAsnGlyGlyGluValTyrArgHisAspAspGl GITCGIATGGITATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCA **ATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGC** ----AlaprolleSerAsnSerAsnArgAlaSerPr NGAAATCGAGAGTGTGCTCTCCCCGGCAGGCCTGAGAATGAGTGGGAATC LysAspGlySerAla--------LeuGluLysMetAspGl TATGGCAAACTCAAGGAGGAGGAACTTCTTTGGTCCC---SerSerAspTyrLys-------STACCAAGAGCCAGACCCCTGAT-----::: []e-----ICA 1588 ler 847

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                                                        3.65e-11
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Query Match:
DB:
C,Genetics:
A,Gene: F19C24.19
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Qy	λ̈	qa	ΟŻ	οp	δŏ	qq	δλ	qq	δy	QQ	δ	qq	δŏ	Dp	δy	DP	δ	qq	ò	ПЪ	ζŏ	ДŪ	٥٨	Ор	ζ)	QQ	72	Ωp	λŏ	QQ	δλ	QQ	RESULT	hypoth

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closis, A.; Bcker, V.R.; Pallm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Fe 408, 816-820, 2000
to A. Sac, Carlon, A.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, M.; Rooney, T.; Rowley, D.; Sakano, H.
Anors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
He: Sequence and analysis of chromosome i of the plant Arabidopsis.
ession: C86275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s-references: GB:AE005172; NID:g5080792; PIDN:AAD39302.1; GSPDB:GN00141
: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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122 AspMetValValAlaAspAlaAspGlnAspAspAspAspAspAspAspAspLeuGly
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US-09-270-437D-5 (1-1708) x T27855 (1-768) 131 GGGCGCGGGGGGCTTTGGCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCG 190 131 GGGCGCCGAGGGGGCTTTGGCTCTCGGGGTCAGCCCCCCCC	266 ATTGGCAAGGAGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGAC 325 280 IleGlyLysGlyGlySerGluIleArgLeuIleGlnGlnThrSerGlyCysArgValGln 299 326 GTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCT 385 ::: 300 MetAspProAspHisGlnSerValAsnGlyPheArgAsnCysThrIleGluGlyProPro 319	386 GAGGGCTGCTCCTGTGTAAGATGATCTTGGAGATTATGCATAAAGAG 436 320 AspGlnValAlaValAlaArgGlnMetleThrGlnValIleAsnArgAsnGlnThrGly 339 437 GCTAAGGACACCAAAACGGCTGACGGTTCCCCTGAAGATCCTGGCCCATAATAACTTT 496	IleGiyLeuvaliieGiyLysGlyGiyGluThrIleArgIlevaiGlnGluGlnGluGlnSerGl ACAAAATCACCATCTCTCGTTGCAAGACCTTACCCTTTACAACCC :::	559 LeuargmetileGlyserFroalaalaileGluinfAlaLysAlaLeuvalHisAshile 418 665 ATGAAGAAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCCATGAGCTCTCACCTGATC 724	CCTCCCAGCAGCGTTACTGGGGCTCCTTATATGCAGGCTCCCGAGCAGCCCCGAGCAGCTCCCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	GAGCACATCAAACAGCTTTGCCAGCGCTCCATCAAGATTGCCGCAAACAGCTTTGCCAGCAGCGCTCCATCAAGATTGCCACCAAAAAAGLGAAAAAAAAAA	965 ACACCTGACTCCAAAGTTCGTATGGTTATCACTGGACCCCCAGAGGCCCCAATTCAAG 1024 491 ASDPLOASHSErGluAspArgileAlaValileMetGlyThrArgAspGlnIleTyrArg 510 1025 GCTCAGGGAAGAATCTATGGCAAACTCAAGGAGCGAGAACTTCTTTGGTCCCAAG 1078
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228 Hisleu	932 GCCAGCCCTCCATCAAGATTGCACCCCGAAACACCTGACTCCAAAGTTCGTATGGTTT		GTACCAAGGACCCGGACCCTGATGAGAACGACCAGGTCATCGTGAAAATCATC ::::: ::: ::: LeuGlnLysGluAspValProLysIleAlaArgGluAspGluGluMetValGlnIleThr GGACATTTCTATGCCAGTCAACGGAAGATCCGAGACATCCTGGCCCAGGTT ::: :::		hypothetical protein ZK418.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: D5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27855 R;Fulton, L. submitted to the EMBL Data Library, April 1994 A;Description: The sequence of C. elegans cosmid ZK418.	A; Accession: T27858 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-768 <ful> A; Cross-references: EMBL:U00047; PIDN:AAA50693.1; CESP:ZK418.9 A; Experimental source: strain Bristol N2</ful>	Ajdene: CESP: ZK418.9 AjIntrons: 166/1; 221/3; 243/1; 279/1; 387/3; 490/1; 567/3; 727/2 Alignment Scores: 6.59e-10 Length: 768 Score: 248.00 Matches: Percent Similarity: 37 89% Mismatches: 225 Query Match: 22.66% Mismatches: 134 DB: 27.97% Gaps: 22.66%

us-09-270-437d-5_1.rpr

71 AACCATGCCTGAAGGTCTCCTACATCCCGATGAGCAGATAGCACAGGGACCT 124	66ProLeugluAspGlnProAspAlaLysLysValAlaProGlnAsnAspSer 194GCCCCAGCCAAGCAGCAGCAAGTAGACATCCCCCTTCGG	233 CTCCTGGTGCCACCCAGTATGTGGTTGCCATTGGCAAGGAGGGGGCCACCATCGC 292 105 TyrLysVallPl 105 TyrLysVallPl 105 TyrLysVallPl 106 TyrLysVallPl 107 TyrLysVallPl 108 TyrLysVallPl 108 TyrLysVallPl 109 AACATCACAAAACAGCCCAGTCCAAGATAGCGTGCATAGGAAGGA		461 184 518	204 GlyGlyGluThrIleLysGlnLeuGlnGluArgAlaGlyValLysMetValMet 221 578 TTGCAAGACCTTTACCACTGAGAGGACCATCACTGTG 622 :::	623 AAGGGGCCATCGAGAATTGTTGCAGGCCGAGCAGAAATAATGAAGAAGTTCGGGAG 682	728 GGCCTGAACCTGGCTGCTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCT 787 269	788 270 848	277 GlylleAspValProlleFroArgPheAlaValGlylleValileGlyArgAsnGlyGlu 296 908 CACATCAAACAACACTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAA 964 297 MetileLysLysIleGlnAsnAspAlaGlyValArglleGlnPheLySProAspAspGly 316 965ACACCTGACTCCAAAGTTCGTATGATGATCATCATCACTGGACCGCCAGAGGCCCAA 1018	11700 A)D144A04011011111111111111111111111111111
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Db 531 AspArgGlySerAlaGlyThrValLeuProGlyGlnSerIlePheTyrMetHisValPro 550 Qy 1115 GCATCAGCCGGTCATTGGCAAAGGTGGAAAACGGTGAACGAGTTGCAGAAT 1174	1280 CGGAAGATCCGAGAGATC	Qy 1297	1337 AACCAGGCCCAGGCAGGAAGTGACCACCCCTCCCTTCTTTGAGTCCAGGACA 1337 AACCAGGCACAGAGAAGTGACCACCCCTCCCTTTTTTTTT	OMETGINGINDFOGLINALASEIVALILEPrOGLINALASERALAASPPROALAPROALAVA CCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGGCTGTAGATCAGGT :::	OY 1487 TIGCCCACTIONITEDGRADGETICCAGIGAGGACCCIGATC 1531 Db 728 erileGlyLeuvalGluGinalaAlaMetValGluSerGlnMetArgArgArgAsnGlnSer- 747 Qy 1532 TNTCAGCCCCAACACCCCATTGGCCCACTGTNTGCCCTTCG 1581 Db 748AShTHRAIAPPOGLUGIYASDVALSERGIYVALFROGIN 760	RESULT 6 A3184 myc far upstream element-binding protein - human N'Alternate names: FVB2-binding protein C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999	C.Accession: A33184 R.Duncan, R.; Bazar, L.; Michelotti, G.; Tomonaga, T.; Krutzsch, H.; Avigan, M.; Levens Genes Dev. 8, 465-480, 1994 A.Title: A sequence-specific, single-strand binding protein activates the far upstream A.Reference number. B53184. MITD. 84170491.	A; Accession: A53184 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-644 < DUN> A; Cross-references: GB: U05040; NID: g460151; PIDN: AAA17976.1; PID: g460152 C; Keywords: DNA binding	Alignment Scores: 1.22e-09 Length: 644 Score: 244.00 Matches: 148 Score: 36.46\$ Conservative: 93 Best Local Similarity: 22.39\$ Mismatches: 219 Query Match: 2.39\$ Indels: 202 DB: 2.39\$ Gaps: 33	US-09-270-437D-5 (1-1708) x A53184 (1-644)

A; Residues: 1-680 < SCH> A; Cross-references: EMBL: U88174; PIDN: AAB42272.1; GSPDB: GN00019; CESP:MOIAIO.1 A; Experimental source: strain Bristol N2; clone MOIAIO C; Genetics: Strain Bristol N2; clone MOIAIO C; Genetics: A; Gene: CESP: MOIAIO.1 A; Map position: 1 A; Map position: 1 A; Introns: 63/2; 97/3; 121/1; 160/1; 269/3; 411/3; 512/1; 649/2 Alignment Scores: 2.23e-09 Length: 680 Score: 240.50 Matches: 82 Percent Similarity: 41.21* Conservative: 82 Best Local Similarity: 20.00* Mismatches: 75 Onery Match: 7.73* Indels: 75	2 Gaps: 12 -270-437D-5 (1-1708) x T25832 (1-680) 104 GAGCAGAGAGACCTGACAATGGCGCCGAGGGGGCTTTGGCTCTCGGGGTCAG 16 ::: ::: 97 LysHisIleSerSerSerThrAspThrAlaArgLysAxgAspPheAspGluArgSer 11 164 CCCCGCCAGGCCTCACCTGTGGCAGGGGCCCCAGCCAAGCAGCAGGAGTG 21 :::	Db 116GludlySerAspGludYrGluGAuTyrAlaProFroCysLySLeuInTLySGLY 133 Qy 218 GACATCCCCTTCGG	174 365 193 425 213	Qy 443GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAAC 493	
Qy 1019 TTCAAGGCTCAG	393 ĠİyİyşcilyĞIYÜHİTİLELYSSETILESErĞINĞINSERĞIYĞİARIŞILEĞINLEU 1199 CCAAĞĞACCAĞACCCTĞATĞAĞAACGACCAĞĞTCATCGTĞAAATCATCĞĞACAT	Oy 1297 CCTGGCCCAGGTTAAGCAGCATCAGAAGGAAGTAACCAGGCCAGGCAGG	Qy 1395		RESULT 7 T25832 Hypothetical protein MO1A10.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T25832 R;Scheet, P. Submitted to the EMBL Data Library, February 1997 A;Description: The sequence of C. elegans cosmid MO1A10. A;Reference number: Z20094 A;Accession: T25832 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

	Cy 158 GGTCAGCCCGCCAGGGCTCACCTGTGGCAGGGGGGGCCCCAGCCAG	AAGCAGCAG 211
Oy 997 CACTGGACGCCAGAGGCCCAATTCAAGGCTCAAGGAAAGAATCTATGGCAAACTCAAGGA 1056	212	0
1057 GGAGAACTTCTTTGGTCCCAAGGAGAAGAGAAGAGAGAGA	Db 39 AspArgAspSerLeuVallleAspArgAspAspThrValPheArgTyrLeuCysProVal	TyrLeuCysProval 58
424 GlyTyrGlyGlnAlaGlyGlnGlyTyrGlnGlnAspGlyTyrGlyAlaTyrAsn	Qy 248 CAGTATGTGGGTGCCATTATTGGCAAGGAGGGGGCCACCATCGGCAACATCACAAAACAG :::::::::::::::::::::::::::::	AACATCACAAAACAG 307 ::: Glulanaraasaa 78
1117 ATCAGCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTT	308	
442 AlaSerGInGlnSerGIyTyrGlyGln	Db 79 ThrargSerLyslleArglleGlyGluAlalleProGlyCysAspGluArgVallle	::: AspGluArgValIle 97
odcoccacticacoi	(2) 368 AGTGTGCACCTCCACCCTGAGGGCTGCTGCTCCTCCTCT	GAGGCTGCTCCTCC 400
Qy 1234 CATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGA 1293	90 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
472AlaSerGinAlaAlaPro	::: :::	 AspAspAlaArgSer 137
OY 1294 CATCCTGGCCCAGGTTAAGCAGCAGCAAAGAGAGAAAAGAAAAGAGAAAGAA		
1354 GAGGAAGTGACCAGCCCTCCCTTNGAGTCCAGGACAACAAGGGCAGAAATCG	Db 138 GluAspSerProGluGlyGluLysGlnValThrAlaLysLeuLe Qy 497 GTAGGGCGTCTCATTGGGAAGGAAGGAACCTGAAGAAGG	ValProSerAspGin 157 GAGCAAGATACCGAG 556
492 yGlnGlnProProAlaGlnGlySerThrGlyGlnAlaGlyTyrGlyAlaProProThrSe	Db 158 IledlyCysIleLeuGlyArgGlyGlyGlyGlnIleValGlnAsnIleArgSerGluThrGly	::: ArgSerGluThrGly 177
OY 1414 AGAGTGTGCTCCCCGGCAGGCCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGG 1473 :::	Oy 557 ACAAAAATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGGGGGGGGGGGGGGGGGGGGGGGGG	TACAACCCTGAGAGG 610 ::: aLeuAsnSerAspGlu 197
Qy 1474 CTGTAGATCAGGTTTGCCCACT 1495	611	
354 OFLOGIASCILLY SFIOFICIAL SS	Db 198 LeulleGlnIleSerGlyGluValLeuIleValLysLysAlaLeuLeuGlnIleAlaSer	LeuGlnIleAlaSer 217
n F8M21.160 - Arabidopsis thaliana sis thaliana (mouse-ear cress)	OY 671 AAAGTTCGGGAGGCCTATGAGAATGATGGCTGCCATGAGCTCTCACCTGGTCCTGGC ::::::	CACCTGATCCCTGGC 730 ::: danleu 229
one trext_change or can to the	Qy 731 CTGA	AGTCCCGCCGCCTCCC 790
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S. submitted to the Protein Sequence Database, April 2000	Le Db 230LeuSerSerGlyGlyTyrProAlaGlySerLeuMetSerHisAlaGlyGly	SerHisAlaGlyGly 247
A;Accession: T49962 A;Accession: T49962 A;Status: preliminary	791	
A;Molecule type: DNA A;Residues: 1-568 <bev></bev>	248 FroArgu	
A;Cross-references: EMBL:AL353993; GSPDB:GN0063; ATSP:F8M21.160 A;Experimental source: cultivar Columbia; BAC clone F8M21 C:Generics	Oy 824TITATGCAGGCTCCCGAGCAGGAGGATGGTGCAGG	ATGGTGCAG 856 ::::: :GluphephelleArq 287
A;Gene: ATS: FBM21.160 A;Map position: 5	857	
A;Introns: 200/3; 337/3; 544/3	bb 288 LeuValSerProValGluAsnIleAlaSerValIleGlyLysGlyGlyAlaLeulleAsn	 GlyAlaLeuIleAsn 307
9 Length: Matches:	QY 917 CAGCICTCCCGGTITGCCAGCGCCTCCATCAAGATIGCACCACCGGAAACACCTGGAAACACTGGAAAACACTGGAAAACACTGGAAAACACTGGAAAAAAAA	
nt Similarity: 42.47% Local Similarity: 20.67%	Db 308 GlnieuArgGlnGluThrArgAlaThr1leiysValAspSerSe	argihrGluGlyAsn 327
uery Match: 7.54% Indels: 2 Gaps:	716	
US-09-270-437D-5 (1-1708) x T49962 (1-568)	Db 328 AspCysLeulleThrIleSerAlaArgGluValPheGluAspAlaTyrSerProThrIle	TyrSerProThrile 347
98 CCCGATGAGCAGATAGCACAG	OY 1010 GAGGCCCAATTCAAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTT	
		ıArgAspSerGlyLeu 367
	Qy 1070 GGTCCCAAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGC	AGCATCAGCAGCTGGC 1129

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i é	. ע פרע	λō	626
ò	TCAGAAATTNTAGCGCAAGGCACTTTTAAACGTGGATTG 16	qa	208
3 8	: 526 AlaGlnMetLysLysLysA	ð 6	9 6
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qq	546IledinGlnMetBroMetGlyMetAlaMetProGln 557	qa	241
RESULT T19217	•	δ	806
hypothe C;Speci	elegans	q	244
C;Date: C;Acces	<pre>C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C.Accession: T19217</pre>	ò	998
R;McMur submitt	ray, A. ed to the EMBL Data Library, June 1996	ପ୍ର	256
A;Refer A;Acces	ence number: Z1909Z sion: T19217	ò	926
A;Statu A;Molec	A;Status: preliminary; translated from GB/EMBL/DDBU A;Molecule type: DNA	ପୁ	276
A, Resid A, Cross	lues: 1-611 <w1l> references: EMEL: Z73969; PIDN: CAA98233.1; GSPDB:GN00023; CESP:C12D8.1b</w1l>	ò	986
A; Exper C; Genet	imental source: clone cizus	οg	296
A, Gene: A, Map p	CESPICIZDB.ID cestion: 5	ò	1046
A; intro	ons: L81/3; 340/3; 535/2	qq	316
	Scores: 8.95e-09 Length:	δ	1082
Score: Percent	232.00 Matches: 37.15% Conservative:	අු	336
Best Local Query Match	ty: 18.75* 7.46%	ò	1139
DB:	sdes z	qu	356
US-09-2	D-S (1-1708) x T19217 (1-611)	79	1199
λō	CCAGCCAAGCAGCAAGTGGACATCCCCTT	d d	376
ag	ProAlaLysArgProAlaAspAspInrAspLeuAsnFroPheMetAspAspAsnGluALa 69	λō	1244
ð í	230CGGCTCCTGGTGCCCACCCAGTATGTGGGGTGCCATTATTGGCAAGGAGGG 280	qa	396
an .	ValASnGluLySiyrFrolieFroctuserAlavalGly11eVallieGLyAlyGly	ò	1304
8 1	GCCACCATCCGCAACATCACAAAACAGACCCAGGTCCAAGATAGACGTGCATAGGAAGGA	අු	414
an i	Sergini reginary reginary saragiyy sargyardinarsar rioaspara	ò	1364
à i	AACGCAGGIGCAGCIGAAAAAGCCAICAGIGIGCACICCACCCCTGAGGGGIGCICCICC 40	a	430
g G	AspProSerSerGlyValArgMetValInrLeuGluGlySerArgSerAsnValGluInr	ò	1424
È	GCTTGTAAGATCTTGGAGATTATGCATAAGAGGCTAAGGACACCAAA	qa	449
셤	AlaLysHisLeulleAsnGluValValAlaArgSerGlnAsnProArgProGlnTyrGly	δ	1460
Š	Acgertgacgacgatccccrgaadarccraraaraaratrasascsrcrc	අු	469
gg	PheProArgAlaGininrileAspileAlalieFroFroBanargCySGlybeule	ò	1490
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50 -------ACACNTGGGCCGGGCTGTAGATCAGGTTTG----- 1489
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|0 ---SerAlaProAlaGlnAsnAsnPheGlyGlyGlnGlnTrpAsnProValAlaGln 448
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| AlaGlnGlnThrAlaAlaProAlaAlaProTyrAlaAlaAlaGly1leValGlnPro 488
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                              GGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCC 685
                                                                                                               ATCTCCTCGTTGCAAGAC --- CTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAG 625
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Db 149 ArglleLysGlnThrLeuProSerSerProThrThrLysSerSerProSerAspPro Qy 470 CTGAdGATCCTGGCCCATAATAACTTTGTAGGCGT :::		683 248	Oy 695 Db 268	QY 7.10 AGCTCTCACTGATCCCTGGCCTGAACCTGGTGTTTCCCA		QY 761	OY 776 GTCCCGCCGCCTCCCAGCGTTACTGGGGCTGCTCCTATAGCTCCTTATGCAGGCT 835	OY 836 CCCGAGCAGGAGATGGTGCAGGTGTTTATCCCGGCCCAGGCAGTGGGCGCCATCATGGGC 895	QY 896 AAGAAGGGCAGCATCAAACAGCTCTCCCGGTTTGCCAGGGCCTCCATCAAGATTGCA 955	Qy 956 CCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACCTGGACCGCCAGAGGCC 1015 Db 395 ThralaalaThrasnGly 400	OY 1016 CAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTC 1066	Oy 1067 TITGGICCCAAGGAAGTGAAGCTGGAGACCCCACAIACGTGTGCCAGCATCAGCAGCT 1126	Qy 1127 GGCCGGGTCATTGGCAAAAAGGTGAACGTGAAGGTTGCAGAATTTGACGGCAGCT 1186	Qy 1187 GAGGTGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGTCATGTG 1240	Qy 1241 AAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAA 1279
508 1553 528 1586 548	1625 TTTAAAGAAGCTCTCC ::: 56811eG1 ULT 12	OnCOMBOUNTAL VEHITAL ANTIGEN-1 - human C.Species: Homo sapiens (man) C.Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999 C.Accession: I38489 R.Buckanovich, R.J.; Posner, J.B.; Darnell, R.B.	Neticil. 1, 637-972, is paraneoplastic Ri Antigen, is Homologous to an RNA-Binding Protein an A/Reference number: 138489; MUID:94000830; PMID:8398153 A/Accession: 138489	A,Molecule type: mRNA A,Residues: 1-510 «RES> A,Cross-references: EMBL:U04840; NID:g440877; PIDN:AAA16022.1; PID:g440878 A,Genetics:	Alignment Scores:	Fred. No.: 4.92e-08 Length: 510 Score: 221.50 Matches: 111 Percent Similarity: 34.89\$ Conservative: 68 Best Local Similarity: 21.64\$ Mismarches: 123	7.12% Indexs:	125 GAGAATGGGCGCCGGAGGGCTTTGGCTCTCGGGGTCAG	164 29	221ATCCCCTTCGGCTCCTGGTGCCACCCAGTATGTGGGTGCCATTATTGGCAAGAGAGAG		338 GAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGGCACTCCACC ::::::		AAAGAGGCTAAG	

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evolutionarily conserved motif
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|LeuArgLeuValValProAlaThrGlnCysGlySerLeuIleGlyLysGlyGlyCysLys 119
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80 GluGluAspileAsnSerSerMetThrAsnSerThrAlaAlaSerArgProProValThr 99
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hnRNP protein - African clawed frog
hnRNP protein - African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: S41224
R;Sioni, H., Matunis, M.J.; Michael, W.M.; Dreyfuss, G.
Nucleic Acids Res. 21, 1193-1198, 1993
A;Title: The pre-mRNA binding K protein contains a novel evolutionarily cons
A;Reference number: S41224; MUID:93219080; PMID:8464704
                                                                                                                                                                                         590 ACCCITACAACCCIGAGAGCACCAICACIGIGAAGGGGCCCAICGAGAAITGITGCAGG
                                                                                                                                                                                                                                                                     GCCGAGCAGGAAATA------ATGAAGAAAGTTCGGGAGGCCTATGAGAATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: transformation upregulated nuclear protein HNRPK
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A, Molecule type: mRNA
A, Residues: 1-396 <SIO>
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A, Residues: 1-204,'V', 206-356 < LEF>
A, Cross-references: EMBL:X78137; ND19460770; PIDN:CAA55016.1; PID:g460771
A, Oross-references: EMBL:X78137; ND19460770; PIDN:CAA55016.1; PID:g460771
A, Noce: submitted to the EMBL Data Library, March 1994
B, Aasheim, H.C.; Loukianova, T.; Deggerdal, A.; Smeland, E.B.
Nucleic Acids Res. 22, 959-964, 1994
A, Title: Tissue specific expression and cDNA structure of a human transcript encoding A, Reference number: $43489; MuID:94203810; PMID:8152927
                                                                                                                                                                                                                                                                                                                                                                                                                                    each
                                               alpha-complex protein 1 - human
N.Alternate names: nucleic acid-binding protein; protein PCBP-1
C.Species: Home sapiens (man)
C.Species: Home sapiens (man)
C.Accession: S58529; S58523; S65678; S43489; S41378; S42472
C.Accession: S58529; S58523; S65678; S43489; S41378; S42472
S.Kiledjian, M.; Wang, X.; Liebhaber, S.A.
ENBO J. 14, 4357-4364, 1995
A;Title: Identification of two KH domain proteins in the alpha-globin mRNP stability (M. Receion, eccept)
A.Reference number: S58523; MUID:96016208; PMID:7556077
                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Nolecule bype: protein
A;Nolecule bype: protein
B;Nolecule bype: polyard, K.; Celis, J.E.
Eur. J. Biochem. 230, 447-453, 1995
Eur. J. Biochem. 230, 447-453, 1995
A;Title: Charactersization of two major cellular poly(rC)-binding human proteins, by Reference number: 865678; MUID:95331278; PMID:7607214
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A,Cross-references: EMBL:Z29505; NID:g444020; PIDN:CAA82631.1; PID:g444021
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A,Cross-references: GDB:344947
C,Keywords: RNA binding
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 1.356 < Kit.>
A, Accession: S58528
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l Similarity: 22.7 ch: 6.99	US-09-270-437D-5 (1-1708) x S41224 (1-396)	221 ATCCCCTTCGGCTCCTGGTGCCCACCCATATGTGGGTGCCATTATTGGCAAGGGG 280 :::	281 GCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGGAAGGA	60 LysAsnileLysAlaLeuArgThrAspTyrAsnAlaSerValSerValPro 76	341 AACGCAGGTGCAGAAAAAGCCATCAGTGTGCACTCCACCCTGAGGGCTGCTCCTCC 400	77 AspSerSerGlyProGluArgileLeuSerileSerAlaAspIleGluThrIleGlyGlu 96	401 GCTTGTAAGATGATCTTGGAAGATTATGCATAAAGAGGCTAAAGGACACCAAAACGGCTGAC 460	97 IleLeuLysLysIleIleProThrLeuGluGluHisPheLysGlyAsnAspPhe 114	461 GAGGITCCCCTGAAGAICCTGGCCCATAATAACTITGTAGGGCGTCTCAITGGCAAGGAA 520			581 CAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCCATCGAGAAT 640	153 GlnGluCysCysProHisSerThrAspArgValValLeulleGlyGlyArgProAspArg 172	641 TGTTGCAGGCCGAGCAGCAATAATGAAGAAGTTCGGGAGGCCTATGAGAATGATGTG 700	173 ValValGluCysIleLysVallleLeuAspLeuIleSerGluSerProVal 189	701 GCTGCCATGAGCTCTCACCTGATCCCT727		728	210 ThrMetMetPheAspAspArgArgGlyArgProHisGlyPheSerMetHisAlaArgGly 229	752 CTITICCCAGCTICATCCAGCGCAGTCCCGCCGTCCCAGCAGCGTIACTGGGGCTGCT 811		242 -ProMetProGlnSerArgArgAspTyAspAspAspAscAr 256	872 CAGGCAGTGGGCGCATCATCGGCAAGAGGGGGCACATCAAACAGCTCTCCCGG 928	256 gArgGlyProLeuProProProGlyArgGlyGlyArgGlyGlyGrArgAlaArgAs 276	929 TITGCCAGCGCCTCCATCAAGAITGCACCACCGGAAACACCTGACTCCAAAGTTCGTATG 988	276 nLeubroLeuProProProProProArgGlyGlyAspArgArg 291	989 GITATCATCACTGGACCGCCAGAGGCCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAA 1048	292GlyArgProAspHisTyrAspGlyMetGlyGlyArgGlyArgGlyArg 307	1049 CTCAAGGAGAACTTCTTTGGTCCCAAGGAAGTGAAGCTGGAGACCCCACATACGT 1108	308 GlySerPheGlyAspIleGlyGlyFroVallleThrThrGlnValThr 323	1109 GTGCCAGCATCAGCAGCTGGCCGGTCATTGGCAAAGAGGAGAAAACGGTGAACGAGTTG 1168 :::
Best Que: DB:	us-	Sy Bp	ò	q _C	δλ	Ор	δy	Ор	දි දි	ò	다. 다.	δλ	qq	ò	qq	ò	Op Op	ò	QC	6 G	5	QQ	δ	Db	ά	Dp	ολ	qq	δ	Op	65 DP

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Alternate names: protein - Arabidopsis thaliana
NiAlternate names: protein T32N21.30
NiAlternate names: protein T32N21.30
NiAlternate names: protein T32N21.30
NiBace: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
NiAcession: T46439
NiAcession: T46439
NiBacesion: T46439
NiAcession: T46439
1169 CAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGAGCAGACCAGACCTGATGAGAACGAC 1228
                                                                                               1229 CAGGICAICGIGAAAAICAICGGACAITITCTAIGCCAGICAGAIGGCTCAACGGAAGAIC 1288
                               344 ArgHisGluSerGlyAlaSerIleLysIle-----AspGluProLeuGluGlySerAsp 361
                                                                                                                              260 GCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAG 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 ServallleGlyLysGlyGlyGlySerThrlleThrGluPheGlnAlaLysSerGlyAlaArg 67
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Experimental source: cultivar Columbia, BAC clone T32M21
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Introns: 29/1; 108/3; 144/2; 209/1; 229/3; 261/3; 282/2;
Note: T32M21.30
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CASATES M.B., Bonaldo M.F., Casavant T.L., Scheetz T. E.,

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CANDER S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

CANDER S.A., McEwan P.J., McKernan M., Madan A., Gay L.J., Hulyk S.W.,

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Davis-Smyth T., Duncan R.C., Zheng T., Michelotti G., Levens D.;
The far upstream element-binding proteins comprise an ancient family of single-strand DNA-binding transactivators.";
J. Biol. Chem. 271:31679-31687(1996).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NGBI_TaxID=9606;
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096124; 022946; 03BVB6; 03BVB6;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 3 (FUSE binding protein 3).
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                               PCB2_HUMAN
ROK_ADATH
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PCB2_MOUSE
PPD2_YEAST
S160_YEAST
TDMH_HUMAN
YAV2_XANCY
WAPA_HUMAN
WAPA_HUMAN
WAPA_HUMAN
GLT0_WHEAT
BATC_HUMAN
GLT5_WHEAT
RATT_RATT
BBN6_EBV
ZICS_HUMAN
STRS_HUMAN
STRS_HUMAN
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                                                                         Compugen Ltd.
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                               244
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                                                                                                                                                                                   CAGACCCAGTCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCC 364
                                                                                                                                                                                                                                                                                                                                                                        :::
145 ValAspArgCysArgAsnGlyProGlyPheHisAsnAspIleAspSerAsnSerThrlle 164
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321 IleLeuThrAlaGlnGluArgAspGlyPheGlyGlyLeuAlaAlaAlaArgGlyArg--- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAIGIGGCIGCCAIGAGCICTCACCIGAICCCIGGCCIGAACCIGGCIGCIGIAGGICIT 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 GlyvalArgileGlnPheLysProAspAspGlyIleSerProGlu------ArgAla 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 ThrTyrThrValProAlaAspLysCysGlyLeuValIleGlyLysGlyGlyGlyGluAsnIle 377
                                                                  82
                           185 GCAGCGGGGCCCCCAGCCAGCAGCAGCAGTGGACATCCCCCTTCGGCTCCTGGTGCCC
                                                      245 ACCCAGINIGIGGGIGCCAITAITGGCAAGGAGGGGCCACCATCCGCAACATCACAAA
                                                                                                                                 106 GluSerGlyCysLyslleGlnIle---AlaSerGluSerSerGlyIleProGluArgPro
                                                                                                                                                                                                                                                                                         :::|||||||
199 IleGlnAspGlyProLeuProThrGlyAlaAspLysProLeuArgIleThrGlyAspAla
                                                                                                                                                                                                                                                                                                                                             ---CATAAAGAGGCTAAGGACACCAAAACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                        458 GACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                              518 GAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------IleGluvalSerValProArgPhe
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264 AlaValGlyIleValIleGlyArgAsnGlyGluMetIleLySLySIJeGlnAsnAspAla
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                                                                                                                                                                                                                                                             365 ATCAGTGTGCACTCCACCCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::: |||||||||::: 301 AlaGlnValMetGlyProProAspArgCysGlnHisAlaAlaHisIleIleSerGluLeu
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                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 AspProSerValTyrGlyTyrGlyValGlnLysArgProLeuAspAspGlyValGlyAsn 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KH 1.
KH 2.
KH 3.
KH 3.
KH 3.
KH 4.
MABLVQGQSAPVGMKABGFVDALHRVRQIAAKIDSIPHLNN
STPLVDPSVYGYGVGKRPLDDGV -> MPPI (in
                                                                                                                                                                                                                                                       SIMILARITY: Contains 4 KH domains.

ACMTION: Ref.1s equence differs from that shown due to a frameshift in position 18.

CAUTION: Ref.2 (AAH01135) sequence differs from that shown due to a frameshift in position 527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 GAGAACCATGCCCTGAAGGTCTCCTACATCCCCGATGAGCAGATAGCACAGGGACCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| ||| |||:::
27 ArgGlnIleAlaAlaLysIleAspSerIleProHisLeuAsnAsnSerThrProLeuVal
                                             far-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWART, SM00322; KH; s.

PROSITE; PS50084; KH TYPE 1; 4.

Transcription regulation; Trans-acting factor; Nuclear protein;

DNA-binding; Repeat; Alternative splicing.
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May interact with single-stranded DNA from the jupstream element (FUSB). May activate gene expression.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
                                                                                                                                                                                               Isold=Q96124-2; Sequence=VSP 008323; VSP 008324;
Note=No experimental confirmation available;
TISSUB SPECIFICITY: Detected in a number of cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP 008323.
Missing (In isoform 2).
/FTId=VSP 008324.
/FTID=VSP 008324.
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Matches:
Conservative:
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Indels:
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                                                                                                                                                            IsoId=Q96I24-1; Sequence=Displayed;
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EMBL; BC001325; AAH01325.1; ALT_FRAME.
EMBL; BC007874; AAH07874.1; -.
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InterPro; IPR004088; KH_type_1.
Pfam; PF000013; KH; 3.
SWART; SM00322; KH; 3.
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61640 MW;
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37.37%
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Best Local Similarity:
Query Match:
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253
354
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DOMAIN
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VARSPLIC
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1160 AACGAGTIGCAGAATTIGACGGCAGCTGAGGTGGTAGTACCAAGAGACCCAGACCCCTGAT 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .352 CGGAGGAAGTGACCAGCCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACGGGCAGAAAT 1411
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TISSUE-Retina;

MACHINE-2388257; PubMed=1247932;

Altachus Fachina;

Altachus F., Feingold E.A., Grouse L.H., Derge J.G.,

Altachus R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachus R.F., Jordan H., Bouerow K.H., Schaefer C.F., Bhar N.K.,

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Botheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakernan K.J., Malek J.A., Gunaratne P.H.,

Raha S.S., McWany D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Altalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Raha S.C., Gilmwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,

Rotriguez A.C., Gilmwood J., Schmutz J., Myers M.A.;

Rothnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Rutterfield Y.S.N., Krzywinski M.I., Skalsku J., Smallus D.E.,

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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                            378 LysSerIleAsnGlnGlnSerGlyAlaHisValGluLeuGlnArgAsnProProProAsn 397
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477 lSerGlyProProAlaPheLeuThrGlnGlyTrpGlySerThrTyrGlnAlaTrpGlnGl
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus. TaxID=10090;
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STREAMSTONE OF 1-268 FROM No. (ISSPERA)

STRAINGE, CATACORD, 63 TISSER-Head,

NEDINES, CATACORD, 63 TISSER-Head,

NEDINES, CATACORD, 63 TISSER-Head,

NEDINES, CATACORD, 63 TISSER-Head,

NEDINES, CATACORD, 63 TISSER-Head,

NEDINES, CATACORD, 63 TISSER, C., SCHORL, C., GORDEN, I., SCHORL, C., PARTER, C., SCHORL, C., COLORNE, I., CANADORD, M., MARINGE, T., BALGO, C., CATAGILE, C., COLORNE, I., CALLER, C., COLORNE, I., CALLER, C., COLORNE, I., CALLER, C., COLORNE, I., CALLER, C., CALLER, C., COLORNE, I., CALLER, C., CALLER, C., CALLER, C., COLORNE, I., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CALLER, C., CAL
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CCGCCTCCAGAGCGTTACTGGGGCTGCTCCTATAGCTCCTTTATGCAGGCTCCCGAG	AsnĠiūGlyIleAspVaiProlieProArgPheAiaVaiĠiyileValiieĠiyArgAsn GGGCAGCACACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCC	311 AspGlyThrThrProAspArgileAlaGlnileThrGlyProProAspArg 327 1013 GCCCAATTCAAGGCTCAG	1031	GTCATTGGCAAAAAGGGTGAACGAGTTGCAGAATTTGACGGCTGAGGTG ::: ::: ::: :::	GluLeuGlnArgSerProProProAsnAlaAspProAsnMetLysLeuPheThrileArg GGACATTTCTATGCCAGTCACATGGCTCAACGGAAGATCCG	447 ValAssiptroLeuglyProFicoValProHisGlyProHisGlyValProGlyPro 464 1348 GGCACGGA	1395	1486 TTTGCCCAACTTGAAAAGATGTTCCAGTGAGGAACCCTGATCTNTCAGCCCCAAAC 1545 ::: ::::::
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------TCAGTGGGAAGAAAATAAAATTTCCTTCA 1698
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X MEDLINE=22388227; Pubmed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusha K., Parmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

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Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length
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578 TyrThrLysAlaTrpGluGluTyrTyrLysLysMetGlyGlnAlaValProAlaProAla 597
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                                                                                                                                                                                                                   705. Turker Construction From the Construction of State Construction (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Far upstream element binding protein 1 (FUSE binding protein 1) (FBP) (DNA helicase V) (HDH V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 45-64; 133-145; 271-283; 308-321; 379-386; 414-424 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 191-193; 203-206; 272-279; 284-290; 300-314; 321-328; 394-397; 409-411; 430-438 AND 440-443, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein activates the DNA-binding motif.";
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21127960; PubMed=11222755;
Vindigni A., Ochem A., Triolo G., Falaschi A.;
"Identification of human DNA helicase V with the far upstream
element-binding procesin.";
Nucleic Acids Res. 29:1061-1067(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Leukemia;
MEDIIRE-94170991; PubMed-8125259;
MEDIIRE-94170991; PubMed-8125259;
Duncan R., Bazar L., Michelotti G., Tomonaga T., Krutzsch H., Avigan M., Levens D.;
Avigan M., Levens D.;
R sequence-specific, single-strand binding protein activates upstream element of c-mpc and defines a new DNA-binding motif denes Dev. 8:465-480(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22166132; PubMed=12176931;
Rappsilber J., Ryder U., Lamond A.I., Mann M.;
"Large-scale proteomic analysis of the human spliceosome.";
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                        643 AA
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1663 CACACC----
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                                                                                                                                                                                               MEDLINE=22716800, PubMed=12819782;
Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W.,
Lee S.W., Han J.M., Lue H.-W., Kim S.;
"Downregulation of FUSE-binding protein and c-myc by tRNA synthetase cofactor p38 is required for lung cell differentiation.";
Nat. Genet. 34:330-336(2003).
                                               interacting repressor targets TFIIH to inhibit activated
                                                                                                                                                                                                                                                                                                                                                                                               Isold=096AE4-2; Sequence=VSP 008321;
Note=No experimental confirmation available;
PTM: Ubiquitinated. This targets the protein for proteasome-
INTERACTION WITH SIAHBP1.
MEDLINE=20337922; PubMed=10882074;
Liu J., He L., Collins I., Ge H., Libutti D., Li J., Egly J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50084; KH TYPE_1; 4.
Transcription regulation; Trans-acting factor; Nuclear protein;
DNA-binding; Repeat; UDl conjugation; Alternative splicing;
3D-structure.
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                                                                                              INTERACTION WITH JTV1, UBIQUITINATION, AND PROTEASOME-MEDIATED
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Q - OS (IN REF. 1).
086D4EAAAACF807B CRC64;
                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q96AE4-1; Sequence=Displayed;
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KH 2.
KH 3.
KH 4.
GLY-RICH.
GLY-RICH.
PRO-RICH.
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InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_Cype_1.
Pfam; PF00013; KH; 4.
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EMBL; BC017247; AAH17247.1; -.
PDB; 1J4W; O6-MRA-02.
Genew; HGNC:4004; FUBP1.
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67473 1
                                                          transcription.";
Mol. Cell 5:331-341(2000)
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Qy 1004 CCGCCAGAGGCCCAATTCAAGGCTCAG	1121 GCAGCTGGCCGGTCATTGGCAAAGGTGGAAAACGGTGAACGGTGAATTTGACG 1121 GCAGCTGGCCGGTCATTGGCAAAGGTGGAAAACGGTGAACGGTGAATTTGACG 1181 GCAGCTGAGTAGTACCAAAGGTGGAAAACGGTGAACGACCAGGTCATC 1181 GCAGCTGAGGTGGTAGTACCAAAGAACCACCCCTGATGAGAACGACCAGGTCATC 1181 GCAGCTGAGGTGGTAGTACCAAAGAACCACACCCTGATGAAACGACCAGGTCATC 1181 GCAGCTGAGGTGGTAGTACCAAAGAACCACACCCTGATGAAACGACCAGGTCATC 1181 GCAGCTGAGGTGGTAGTACCAAAGAACCACACCCTGATGAACGACCAGGTCATC 1181 GCAGCTGAGATACCAAAACACACACACCCTGATGAACGACCAGGTCATC 1181 GCAGCTGAGAACAAGAACCACACACCCTGATGAACGACCAGGTCATC	4.06 GIYALGALGGIULGUGIIATGASDRIVIOFIOASDAGAGASDFIOASDAGLUSLGU 4.2 1238 GTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAG 1.2 426 PheThrIleArgGlyThrProGlnGlnIleAspTyrAlaArgGlnLeuIleGluGluLys 4.4 1286 ATCCGAGACATCCTGGCCCAGGTTAAGCAGCATCAGAAGGGACAGAG 1.3	QY	1395CARCACGGGGGGAGAAATCG 1395CARCACGGGGGGAGAAATCG	OY 1474 CTGTAGATCAGGTTTGCCACTTGATTGAGAAGATGTTCCAGTGAGGAACCCTGATCTN 1533 1974	QY 1591 AATTNTAGCGCAAGGCACTTTTAAACGTGGATTGTTTAAAGAAGCTCTCCAGGCCCCACC 1650 :::		cna-binging procein nova-z (neuro-oncological ventral antigen
SAG	Aliange Alia	Db 98 SerValMetThrGluGluTyrLysValPrOAspGlyMetValGlyPheileGlyArg 117 Qy 275 GAGGGGCCACCACACCACACACACACACCCAGTCCAGATAGACGGGTGCATAGG 334 Db 118 GlyGlyGluGhnIleSerArglleGlnGluSerGlyCysLysIleGlnIleAla 136 Qy 335 AAGGAGAACGCAGGTGCAGAAAAAGCCATCAGTGGCACTCAGTCCACCCCAGGGGTGG 394			614ATCACTGAAAGGGGCCATCGAGAATTG 511 ASpLySProLeuArglleThrGlyAspProTyrLysVa 665 ATGAAGAAGTTCGGGAGGCCTA 251 LeuGluleulleArdAspGnGlyGlyGlyBaagagluleul	710 AGCGCAGTCCCGCCGCAGCAGCGCTTGCTTACTCCCTATATG 770 AGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCTATAGCTCCTTTATG	Db 269	

Interru; 200013; KH; 3.
Pfam; PF00013; KH; 3.
PROSITE; PS50084; KH TYPE_1; 3.
Antigen; Nuclear protein; RNA-binding; Repeat; 3D-structure.
DOMAIN 10 26 BIPARTITE NUCLEAR LOCALIZATION SIGNAL

DR DR DR DR DR DR FT FT FT FT FT SQ

A -> R (IN REF. 1). PAA -> TAT (IN REF. 1). 41B63EAF6899256B CRC64;

MW.

49008

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Alignment Scores:

No.:

265 492

CONFLICT CONFLICT

KH 1. KH 2. ALA-RICH. GLY-RICH. KH 3.

99 196 405 393 247

32 130 232 332 247

DOMAIN DOMAIN DOMAIN DOMAIN 492 118 62 1185 15

Length:
Matches:
Conservative:
Mismatches:

6.8e-08 236.50 37.89% 24.84% 7.60%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Indels:

U70477; AAB88661.1; ALT_INIT.

EMBL; AF083898; AAC72355.1; -EMBL; AC006540; AAD13116.1; -PDB; 1DTJ; 18-FEB-00.
PDB; 1EC6; 07-APR-00.
Genew; HGNC:7887; NOVA2.
MIM; 601991; --

InterPro; IPR004087; KH dom. InterPro; IPR004088; KH_type_1

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SEQUENCE OF 29-492 FROM N.A.
Lamerdin J.B., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgecu A., Avila J., Liu S.,
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Brower A., Sanders C., Ow D., Nolan M., Trong S.,
Kobaysahi A., Olsen A.S., Carrano A.V.;
"Sequence analysis of a 1.9 Mb region in 19913.2 between APOE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence specific RNA binding by a Nova KH domain: implications for paraneoplastic disease and the fragile X syndrome."; cell 100:323-3323(2000).

-!- FUNCTION: May regulate RNA splicing or metabolism in a specific subset of developing neurons (By similarity). Binds single strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 405-491 IN COMPLEX WITH RNA. MEDLINE=20139984; PubMed=10676814; Lewis H.A., Musunuru K., Jensen K.B., Edo C., Chen H., Darnell R.B., Burley S.K.;
                                                                                                                                                                                  Louis D.N.;
                                                                                                                                               TISSUE=Brain;
MEDLINE=20197319; PubMed=10735272;
Ueki K., Ramaswamy S., Billings S.J., Mohrenweiser H.W., Louis D.N.;
"ANOVA, a putative astrocytic RNA binding protein gene that maps to
chromosome 19q13.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: Brain. Expression restricted to astrocytes.
DOMAIN: The third KH domain (KH3) recognizes specifically 5'-
                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 405-480.
MEDLINE=99148126; PubMed=10368286;
Lewis H.A., Chen H., Edo C., Buckanovich R.J., Yang Y.Y.-L.,
Musunuru K., Zhong R., Darnel B., Burley S.K.;
"Crystal structures of Nova-1 and Nova-2 K-homology RNA-binding
                                                                                                                                                                                                                                                                                                                                 as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          MEDLINE=99007301; PubMed=9789075;
Yang Y.Y., Yin G.L., Darnell R.B.;
"The neuronal RAN-binding protein Nova-2 is implicated autoantigen targeted in POMA patients with dementia.";
Proc. Natl. Acad. Sci. U.S.A. 95:13254-13259(1998).
(Astrocytic NOVA1-like RNA-binding protein) NOVA2 OR ANOVA OR NOVA3.
                                                                                                                                                                                                                                        Neurogenetics 1:31-36(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structure 7:191-203(1999).
                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                               SEQUENCE FROM N.A.
                                                                           Mammalia; Euther
NCBI_TaxID=9606;
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152 TCTCGGGGGTCAGCCCCCAGGGCTCACCT-----GTGGCAGCGGGGGCCCCAGCCAAG 205
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8 SerArgLysArgProLeuGluThrProProGluValValCysThrLysArgSerAsnThr
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US-09-270-437D-5 (1-1708) x NOA2_HUMAN (1-492)
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DISEASE: Autoantigen in the paraneoplastic opsoclonus myoclonus araxia (POMA), a paraneoplastic neurological syndrome/disorder (PNS/D) associated with breast cancer, fallopian cancer, and SCLCa and characterized primarily by loss of inhibitory control of motor neurons in the spinal cord and brainstem. Recognized by the 1gG autoantibody ANNA-2 (also called anti-Ri).

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Query Match:
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                                                                                               742
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                                                                                                                                                          260 GlyvalGlyAlaPheProAlaAlaLeuProAlaPheSerGlyThrAspLeuLeuAlaIle 279
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|ValGinGluAspProGinSerSerSerCysLeuAsnIleSerTyrAlaAsnValAlaGly 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 sLeu-----AlaAlaGluSerAlaLysGluLeuValGluIleAlaValProGluAsnLe 417
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                                                                                                         280 SerThralaLeuAsnThrLeuAlaSerTyrGlyTyrAsnThrAsnSerLeuGlyLeuGly
                                                                      220 ProValAlaAsnSerAsnProThrGlySerProTyrAlaSerProAlaAspValLeuPro
                                                                                            ----GCTGCCATGAGCTCTCACCTGATCCCTGGCCTGAACCTGGCT
                                                                                                                                                                                                                                                                    895 CAAGAAGGGCAGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGC
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        ---GCCTATGAGAAT----
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Last annotation update)
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                                                                                                                                      743 GCTGTAGGTCTTTTCCCAGCTTC-----
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        GTTCGGGAG-
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[1] -SEQUENCE FROM N.A., SEQUENCE OF 104-119; 242-267; 679-685; 705-711 AND

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

Gallus gallus (Chicken)

NCBI_TaxID=9031;

Gallus.

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743-766, FUNCTION, DEVELOPMENTAL STAGE, AND SUBCELLULAR LOCATION.
MEDLINE=21640447; PubMed=11781334;
Gu W., Pan F., Zhang H., Bassell G.J., Singer R.H.;
Gu W., Pan F., Zhang H., Bassell G.J., Singer R.H.;
A predominantly nuclear protein affecting cytoplasmic localization of beta-actin mRNA in fibroblasts and neurons.";
J. Cell Biol. 156:41-52(2002).
-!- FUNCTION: Binds to a 54-nuclectide localization signal (the zipcode) found in the 3' untranslated region of beta-actin mRNA and may play a role in its localization.
-!- SUBCELLULAR LOCATION: Predominantly nuclear. Also detected in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AlaGluArgGly------ArgArgProProProAlaLeuThrGlyGlyAla
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                                                                                                                                                                                                                                                                                    cytoplasm.
DEVELOPMENTAL STAGE: The highest expression is found in 6-d
embryos, is reduced to 30% before hatching and remains stable
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InterProj IPRUGACO...

R PRART; SM00322; KH; 4.

R PROSTTE; PS50084; KH TYPE 1; 4.

M Transport; mRNA transport; Nuclear protein; RNA-binding; Repr
FT DOMAIN 208 362 KH 2.

FT DOMAIN 296 362 KH 2.

FT TOWAIN 296 362 KH 3.

FT TOWAIN 296 362 KH 3.

FT TOWAIN 296 366 KH 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO, GO:0005737; C:CYCOPISEN; IDA.
GO; GO:0005634; C:DUCleus; IDA.
GO; GO:0003730; F:MRNA 3' UTR binding; IDA.
GO; GO:0008298; P:MRNA 10calization, intracellular; NAS.
INTERPRO; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
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Matches:
Conservative:
Mismatches:
Indels:
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235.50
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7.57%
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Best Local Similarity:
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                                                                       "Cooperative assembly of an hnRNP complex induced by a tissue-specific homolog of polypyrimidine tract binding protein."; Mol. 20:7459-7479(2000).

1. FUNCTION: Binds to the dendritic targeting element and may play a complex that binds to the dendritic targeting element and may play a complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the far-upstream element (FUSE). May activate
                                                                                                                                                                                                                                                                                            and HNRPHI.

SUBCELLULAR LOCATION: Nuclear. A small proportion is also found in the cytoplasm of neuronal cell bodies and dendrites (By similarity).
                                                                                                                                                                                                                                                                               Part of a ternary complex containing FUBP2, PTBP1, PTBP2
                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Detected in neural and non-neural cell lines. SIMILARITY: Contains 4 KH domains. CAUTION: Ref.3 sequence differs from that shown due to numerous
                  MEDLINE=20459250; PubMed=11003644;
Markovtsov V., Nikolic J.M., Goldman J.A., Turck C.W., Chou M.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00322; KH; 4.

PROSITE; PS50084; KH_TYPE_1; 4.

PROSITE; PS50084; KH_TYPE_1; 4.

Transport; mRNA transport; mRNA processing; mRNA splicing;
Transcription regulation; Trans-acting factor; Nuclear protein;
DNA-binding; RNA-binding; Repeat.
DOMAIN 233 299 KH 1.
DOMAIN 233 299 KH 3.

DOMAIN 322 386 KH 3.

Transcription regulation; Transcription;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G -> V (IN REF. 2).
V -> G (IN REF. 2).
G -> GG (IN REF. 2).
G -> A (IN REF. 2).
V -> A (IN REF. 2).
FUNCTION, AND INTERACTION WITH PIBP1; PIBP2 AND HNRPH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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GLY-RICH.
ALA/GLY/PRO-RICH.
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EMBL; AF033747; AAD29861.1; -.
EMBL; AF093745; AAD29861.1; JOINED.
EMBL; AF093748; AAD29862.1; -.
EMBL; U69126; AAC50892.1; ALT_FRAME.
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MIM, 603445,
INCEPEO, IPR004087, KH dom.
InterPro, IPR004088, KH_type_1.
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21.75%
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SUBUNIT: Part o
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707 AA;
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694
                                                            Black D.L.;
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REPEAT
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Percent Similarity: Best Local Similarity:

Query Match: DB:

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183
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|168 nLys1leGlnGlnAspSerGlyCysLysValGlnIleSerProAspSerGlyGlyLeu-- 187
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                                                               AGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTACAT 96
                                                                                                                                                                                                                                                        -----GlyGlyGlyGlyAlaGlyGlyAla 26
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US-09-270-437D-5 (1-1708) x FUB2_HUMAN (1-707)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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EMBL; AV262017; AAP20872.1; ---

DR. InterPro; IPR004088; KH dom.

DR. Pfam; PF00013; KH; 3.

DR. SWART; SW00322; KH; 3.

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WEDLINE=22120219; PubMed=12124753;

Xumar D.V., Nighorn A., St John P.A.;

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Xumar D.V., Nighorn A., St John P.A.;

Xumar D.V., Nighorn A., St John P.A.;

Xumar D.V., Nucleon Specific and neurons.";

Xumar D.V., Nucleon Sequence-specific manner to activate exon inclusion. It binds specifically to the sequence UCAUY (By similarity). Acts to regulate a novel glycine receptor alpha-2 chain splice variant (alpha-2N) in developing spinal cord.

Clain SUBCELLULAR LOCATION: Nuclear.

SIMILARITY: Contains 3 KH domains.
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                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                    breast
                                                                                                                                                                               STRAIN=BDIX, TISSUE-Cerebellum;
Knudsen A., Monstad S.E., Vedeler C.A.;
Nova-1, the paraneoplastic Ri antigen, is associated with
cancer.";
                                                                                                                                                                                                                                                                                  Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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175
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Mismatches:
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432 sLysCysGlyLeuVallleGlyArgGlyGlyGluAsnValLysAlalleAsnGlnGlnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 rGlyAlaPheValGluIleSerArgGlnLeuProProThrGlyThrProThrSerLysLe
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
protein Nova-1 (Neuro-oncological
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                                                                                                                                                                                        GGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGGAAG 337
                                                    GAGAAC-----GCAGGTGCAGCTGAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGC 391
                                                                                88 LysAspPheTyrProdiyThrThrdiuArgValCysLeuIleGlnGlyThrIleGluAla 107
                                                                                                           TGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAA 451
                                                                                                                                      108 LeuAsnAlaValHisGlyPheileAlaĠluLysIleArgGluMetProGlnAsnValAla 127
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LysAlaValGluLeuIleIleGlnLysIleGlnGluAspProGlnSerGlySerCysLeu 226
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1088 AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT 1147
                                                                                     GGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGA--- 1204
                                                                                                                                                                          ---GACCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTAT 1261
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                            Rehbein M., Wege K., Buck F., Schweizer M., Richter D., Kindler S.;
"Molecular characterization of MARTAL, a protein interacting with the dendritic targeting element of MARTAL, a protein interacting with the dendritic targeting element of MARTAL, a protein interacting with the J. Neurochem. 82:1039-1046(2002).

-I- FUNCTION: Part of a ternary complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the faruspaream element (FUSE). May activate gene expression (By similarity). Binds to the dendritic targeting element and may play a role in mRNA trafficking.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a role in mRNA trafficking.
-!- SUBGNIT: Part of a ternary complex containing FUBP2, PTBP1, PTBP2 and HNRPH1 (By similarity).
-!- SUBGELLULAR LOCATION: Nuclear. A small proportion is also found in the cytoplasm of neuronal cell bodies and dendrites.
-!- SIMILARITY: Contains 4 KH domains.
                                                                                                               SEQUENCE OF 73-87; 89-108 AND 475-486, SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                至
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 2 (FUSE binding protein 2)
type splicing regulatory protein) (KSRP) (MAP2 RNA trans-acting protein 1) (MARTAI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00013; KH; 4.

SMART; SM00322; KH; 4.

PROSITE; PSSO084; KH; TYPE_1; 4.

Transport; mRNA transport; mRNA processing; mRNA splicing;

Transcription regulation; Trans-acting factor; Nuclear protein;

DNA-binding; RNA-binding; Repeat.

DOMAIN 145 209 KH 1.

DOMAIN 323 387 KH 2.
                                                                                                                                                                                                                                                                                                                                                                                                   721 AA.
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                                                                                                                                                                                                                                                               1262 GCCAGTCAGATGGCTCAA 1279
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InterPro; IPR004088; KH_type_1.
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LOCATION, AND FUNCTION.
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FUBP2 OR KHSRP
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CCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGAGATGGTGCAGTGTTTATCCCCGCC 87 .:: ::: CAGGCAGTGGGCGCCATCATCGGCAAAAAGGGGCAGCAACAACAACATCTCCCGGTTT 93 .:: ::: ::: HisSerValGlyValValTileGlyArgSerGlyGluMetIleLySLySIleGlnAsnAsp 35 GCCAGCGCCTCCATC	353 AladiyvalargileGinPneLysGinAspaspdiyinTciyProGinLysIcAlahis 372 956CCACCCGAAACACCTGACTCCTAAGTTCGTATGGTT 991	1021CAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGAACTTCTTTGGTCCC 1075 ::: ::::::::::::::::::	1136 ATTGCAAAAGGTGGAAAAACGGTCAACGAGTTGCAGAATTTGACGCCAGCTGAGGTGGTA 1195	AAAATCATGGACATTTCTATGCCAGTCAGGAGAGGTCCAACGGAAGATCCGAGACACCAGAGACACTCAACGGAAGATCCGAGACACTCAACGGAAGATCCGAGACACCAGGTGAAGAGGAAGGA	1355 AGGAAGTGACCAGCCCTCCCTGTCCCTTNGAGTCCAGGACACACACGGCAGAAATUGA	GAGCCCCAAACACCCAATTGGCCCAACACTGTTCAGGGGGGGG	1595 NIAGGGCAAGCCATTITAAAGGIGATITITAAAAGGIGAAGGIGAAGGAGGGIGAAGGAGGAGGAGGAGG
8 8 8 8	8 & 8 & 8	8 8 8	8 8 8	6 6 6 6	6 6 6 6	3 8 8 8 8	CAY DD DD DD DD TESULT TESULT
FT DOMAIN 425 492 KH 4. FT DOMAIN 572 685 4 X 12 AA IMPERFECT REPEATS. FT REPEAT 572 583 1. FT REPEAT 618 629 2. FT REPEAT 644 655 3. FT DOMAIN 7 68 GLY/PRO-RICH. FT DOMAIN 499 613 ALA/GLY/PRO-RICH. FT DOMAIN 499 613 ALA/GLY/PRO-RICH. SQ SEQUENCE 721 AA; 74226 MW, 482C7A765C60EE4A CRC64;	ment Scores: No.: 2.45e-07 1	-09-2/0-43/D-5 (1-1/08) X F0b2_kar (1-/21) 128 AATGGGCGCCGAGGGGGCTTTGGCTCTCGGGGTCAGCCCCGCCAG 128 AATGGGCGCCGAGGGGGCCTTTGGCTCTCGGGGTCAGCCCCGCCAG	ON 191 GGGCCCCAGCCAGCAGCAGCAAGTGGACATCCCCCTTCGGCTCCTGGTGCCCCACCAG 250 191 GGGCCCCAGCCAGCAGCAGCAAGTGGACATCCCCCTTCGGCTCCTGGTGCCCCAG 250 138 IleHisProProProArgThrSerMetThrGluGluTyTArgValProAspGly 155 Qy 251 TATGTGGGTGCCATTATTGGCAAGGAGGGCCCACCATCCGCAACATCACAAAAAGAGC 310 hh 156 MatVafclytarileTlaGlydraTGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	311 CAGTCCAAGATAGACGTGCATAGGAAAAGGTGCAGCTGAAAAAGCCATCAGT 311 CAGTCCAAGATAGACGTGCATAGGAAGGAAAAGCCAGCTGAAAAAGCCATCAGT 176 GlyCysLysValGlnIleSerProAssSerGlyGlyLeuProGluArgSerValSer 371 GTGCACTCCACCCTCAAGGCTGCTCCTCCCCTTGTAAGATGATCTTGGAAGATTATG 111	Qy 428	Oy 518 GAAGGACGGAACCTGAAGAAGGGAAGATACCGAGACAAAATCACCATC 571	Oy 632 ATCGAGAATTGTTGCAGGGCCGAGCAGAATAATGAAGAAAGTTCGGGAGGCCTATGAG 691 133 ValGinGlnAlaCysGluMetValMetAspileLewargGlu 306 Oy 692 AATGATGTGCCATGAGCTCTCACCTGATCCTGGCTGCTGTAGGT 751 Db 307 ArgaspGlnGlyGlyPheGlyAspArgAsnGluTyrGly

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preferentially to oliging dc.
SUBCELLUIAR LOCATION: Loosely bound in the nucleus. May shuttle between the nucleus and the cytoplasm.
TISSUE SPECIFICITY: Abundantly expressed in skeletal muscle, thymus and peripheral blood leucocytes while a lower expression is observed in prostate, spleen, testis, ovary, small intestine, heart, liver, adrenal and thyroid glands.
PTM: PHOSPHORYLAPED. THE NON-PHOSPHORYLATED FORM(S) EXHIBITED THE STRONEST POLY(RC)-BINDING ACTIVITY.
STRONEST POLY(RC)-BINDING ACTIVITY.
CAMPILON: There is probably a frameshift error in the nucleotide sequence of Ref.3.
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lymphocytes;
MBDLINE=94203810; PubMed=8152927;
MBDLINE=94203810; PubMed=8152927;
MBDLINE=94203810; PubMed=8152927;
MBDLINE=94203810; PubMed=8152927;
Tissue specific expression and cDNA structure of a human transcript encoding a nucleic acid binding [Oligo(dC)] protein related to the pre-mRNA binding protein (1994).
Nucleic Acids Res. 22:959-964(1994).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96016208; PubMed=7556077;
MEDLINE=96016208; Liabhaber S.A.;
"Identification of two KH domain proteins in the alpha-globin mRNP stability complex.";
                                                                                                                                        Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                   (Nucleic acid
                                                                                                                                                                                                            MEDLINE=95331278; PubMed=7607214;
Leffers H., Dejgaard K., Celis J.E.;
"Characterisation of two major cellular poly(rC)-binding human proteins, each containing three K-homologous (KH) domains.";
Eur. J. Biochem. 230:447-453(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 601209; -. GO: C: Cytoplasm; NAS. GO: 00055737; C: Cytoplasm; NAS. GO: 00005634; C: mucleus; NAS. GO: GO: 0003723; F: RNA binding; IDA. GO: 0003697; F: Single-stranded DNA binding; IDA. GO: 00016071; P: Single-stranded DNA binding; IDA. GO: 0016071; P: WINA metabolism; NAS.
          PCB1 HUMAN STANDARD; PRT; 356 AA.
013365; Q13157; Q14975;
30-NAY-2000 (Rel. 39, Created)
30-NAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly(rC) binding protein (Alpha-CP1) (hnRNP-E1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH; 3.
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                                                                                                                            sapiens (Human)
                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                      NCBI_TaxID=9606;
PCB1 HUMAN
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427
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120 IleLysGluIleArgGluSerThrGlyAlaGlnValGlnValAlaGly-----AspMet
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                                                                                                                                                                                                                                                                                                                                                                    3 AlaGlyValThrGluSerGlyLeuAsnValThrLeuThrIleArgLeuLeuMetHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 AGTGTGCACTCCACCCCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATG
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|valMetThrileProTyrGlnProMetProAlaSerSerProValIleCysAlaGlyGly
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SMART; SM00322; KH; 3.
PROSITE; PS50084; KH TYPE 1; 3.
Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding;
Phosphorylation; Repeat.
DOMAIN 13 75 KH 1.
                                                                 KH 1.
KH 2.
KH 3.
V -> A (IN REF. 2 AND 3).
W; DC85477576DC5104 CRC64;
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76
74
1138
71
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Matches:
Conservative:
Mismatches:
Indels:
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221.50
41.78%
21.17%
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162
343
205
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205 2
356 AA;
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Best Local Similarity:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 CAAGTGGAC----ATCCCCCTTCGGCTCCTGGTGCCCACCCAGTATGTGGGTGCCATT 265
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                                                                                                                                                                                                                                                  Dredge B.K., Darnell R.B.,
"Nova regulates GABA(A) receptor gamma2 alternative splicing via a
distal downstream UCAU-rich intronic splicing enhancer.";
MOL. Cell. Biol. 23:4687-4700(2003)
--- FUNCTION: Functions to regulate alternative splicing in neurons binding pre-mRNA in a sequence-specific manner to activate exon
binding pre-mRNA in a sequence-specific manner to activate exon
inclusion. It binds specifically to the sequence UCAUY. Most
likely acts to activate the inclusion of exon E3A in the glycine
receptor alpha-2 chain and of exon E9 in gamma-aminobutyric-acid
receptor agamma-2 subunit via a distal downstream UCAU-rich
intronic splicing enhancer.
--- SUBCELIULAR LOCATION: Nuclear.
---- DISERSE: Defects in NOVA1 leads to neuronal death in spinal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIPARTITE NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                  Zhong R., Buckanovich R.J.,
                                                           MEDLINE=20182810; PubMed=10719891;
Jensen K.B., Dredge B.K., Stefani G., Zhong R., Buckanovich
Okano H.J., Yang Y.Y.-L., Darnell R.B.;
Nova-1 regulates neuron-specific alternative splicing and
essential for neuronal viability.";
Neuron 25:359-371(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7D09E8A55B0A7817 CRC64;
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EMBL, AK047565, BAC35988.1; -...
MGJ, MGI.104297; NOVAI...
GO, GO:0005634; C:nucleus; IC...
GO, GO:0003729; F:mRNA binding; IDA...
GO; GO:000371; P:mRNA splicing; IDA...
InterPro; IPR004087; KH-dom.
InterPro; IPR004088; KH-Lype_1.
Pfam; PF00011; KH; 3.
PRART; SM00322; KH; 3.
PROSITE; PS50084; KH-TYPE_1; 3.
Antigner, Nuclear profein; RNA-binding; Repeat...
NON_TER
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Conservative:
Mismatches:
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KH 2.
ALA-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           brainstem neurons.
-!- SIMILARITY: Contains 3 KH domains.
                                                                                                                                                                                                                                      MEDLINE=22692957; PubMed=12808107;
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35.63%
21.66%
7.12%
Nature 420:563-573(2002).
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223
395
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SEQUENCE OF 250-493 FROM N.A.

REQUENCE OF 250-493 FROM N.A.

REQUENCE OF 250-493 FROM N.A.

RA MEDINE=2394683; PubMed=21466851;

RA MEDINE=2394683; PubMed=21466851;

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Tomaru Y., Halla D.P., Bult C., Hume D.A., Concholoch J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Concholoch J.,

RA Baldarelli R., Marapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Baldare J.A., Fretcher C.F., Forrest A., Frazer K.S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Malcati R., Marleais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schanka Y., Taylor M.S., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Magner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pikuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Iroh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa J.,

RA Hara A., Hashizume W., Imotani Y., Ishii Y., Indo H.,

RA Hara A., Hashizume W., Imotani Y., Ishii Y., Indo H.,

RA Hara A., Hashizami Y.,

RA Hara A., Hashizami Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara A., Hashizawi Y.,

RA Hara
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                                                                                                                                                                             ::: ||| ||||||| ::: 317 AsnPro---ValGluGlySerSerGlyArgGlnValThrIleThrGlySerAlaAlaAser 335
                                                                                                                                                    AAGAAGGGGCACACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCA 955
::: ::: ::: ||| ::: ||| 257 PheAlaGlyIleAspSerSerProGluValLysGlyTyrTrpAlaSerLeuAspAla 276
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"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                  336 IleSerLeuAlaGinTyrLeuileAsnAlaArgLeuSerSerGluLysGlyMetGly 354
                                                                CCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCATCATCGGC
                                                                                                         SerThrdlnThrThrHisGluLeuThrileProAsnAsnLeuIleGlyCysileileGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spontaneous mutation in the mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      090776; 080889; 10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) RNA-binding protein Nova-1 (Neuro-oncological ventral antigen 1) (Ventral neuron-specific protein 1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 AA.
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"Neuromuscular ataxia: a new ;
Mamm. Genome 11:820-823(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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NOA1 MOUSE
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SEQUENCE OF 1-34 FROM N.A.
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                     ATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGAC 325
                                                              GTGCATAGGAAGGAGAAC-----GCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCC 379
                                                                                                        380 ACCCCTGAGGGCTGCTCCTCCGCT-----TGTAAGATGATCTTGGAGATTATG 427
                                                                                                                      -----GACACCAAAACGGCTGACGAGTT 466
                                                                                                                                                                                                             131 AspArgIleLysGlnThrLeuProSerSerProThrThrThrLysSerSerProSerAsp 150
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|ProMetThrThrSerArgAlaAsnGlnValLysIleIleValProAsnSerThrAlaGly 170
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                                                                                                                                                                                                                                                                              CGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAA 562
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                                                                                  LeuSerLysSerLysAspPheTyrProGlyThrThrGluArgValCysLeuIleGlnGly 90
                                   31 GlyGluAspGlyGlnTyrPheLeuLysValLeuIleProSerTyrAlaAlaGlySerIle
                                                                                                                                                                      111 GlnAsnValAlaLysThrGluProValSerIleLeuGlnProGlnThrValAsnPro
                                                                                                                                                                                                                                    -----AAGATCCTGGCCCATAATAACTTTGTAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                          -----GCCTATGAGAAT-----
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                                                                       383 GlyTyrPheGlyAlaAlaSerProLeuAlaAlaSerAlaIleLeuGlyThrGluLysSer 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaArgileGlnileSerLysLysGlyGluPheValProGlyThrArgAsnArgLys--- 457
                                                                                                                                                                                                   1124 GCTGGCCGGGTCATTGGCAAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
RNA-Dinding protein Nova-1 (Neuro-concological ventral antigen 1)
(Onconeural ventral antigen-1) (Paraneoplastic Ri antigen) (Ventral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structure 7:191-203 (1999).
-!- FUNCTION: May regulate RNA splicing or metabolism in a specific subset of developing neurons.
-!- SUBCELLUAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P51513-1; Sequence=VSP_002842;
TISSUE SPECIFY: Brain.
DISEASE: Automatigen in the paraneoplastic opsoclonus myoclonus
ataxia (POMA), a paraneoplastic neurological syndrome/disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSP_002843, VSP_002844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99148126; PubMed=10368286;
Lewis H.A., Chen H., Edo C., Buckanovich R.J., Yang Y.Y.-L.,,
Musunuru K., Zhong R., Darnell R.B., Burley S.K.;
"Crystal structures of Nova-1 and Nova-2 K-homology RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUBE-Fetal brain;
Dmitrenko V.V., Garifulin O.M., Shostak K.A., Smikodub A.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1238 GTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAA 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
1013 GCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
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1016 CAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTC------AAGGAGGAGAACTTC 1066
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                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAG--- 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerAsnProThrGlySerProTyrAlaAsnThrAlaGluValLeuProThrAlaAlaAla 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 AlaAlaGlyLeuLeuGlyHisAlaAsnLeuAlaGlyValAlaAlaPheProAlaValLeu 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 SerGlyPheThrGlyAsnAspLeuValAlaIleThrSerAlaLeuAsnThrLeuAlaSer 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 LeuAlaAlaAlaAlaSerAlaAsnProAlaAlaAlaAlaAlaAsnLeuLeuAlaThr 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            896 AAGAAGGGGCAGCACCATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCA 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 TyrpheGlyáláAlaSerProLeuAlaAlaSerAlaIleLeuGlyThrGlúLysSerThr 420
                                 ::: ||| |::: ||| SerLysSerLysAspPheTyrProGlyThrThrGluArgValCysLeulleGlnGlyThr 108
                                                                     TGTAAGATGATCTTGGAGATTATGCAT 430
                                                                                                                                                        AsnValAlaLysThrGluProValSerIleLeuGlnProGlnThrThrValAsnProAsp 148
                                                                                               ValdiuAlaLeuAsnAlaValHisGlyPheIleAlaGluLysileArgGluMetProGln 128
            -GGTGCAGCTGAAAAGCCATCAGTGTGCACTCCACC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GCTTCATCCAGCGCA
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||||||| HetThrThrSerArgAlaAsnGlnValLysIleIleValProAsnSerThrAlaGlyLeu
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328 TyrGlyTyrAsnLeuAsnThrLeuGlyLeuGlyLeuSerGlnAlaAlaAlaThrGlyAla
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                                                                                                                                                                                                                                                ----AAGATCCTGGCCCATAATAACTTTGTAGGGCGT
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                                                                                                                                                                                      -GACACCAAAACGGCTGACGAGGTTCCC
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                                                                        CCTGAGGGCTGCTCCTCCGCT-
                                                                                                                                431 AAAGAGGCTAAG-----
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                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCCGCCAGGGCTCACCTGTGGCAGCGGGCCCCAGCCAAGCAGCAGCAGCAAGTGGAC--- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ATCCCCCTTCGGCTCCTGGTGCCCAAGTATGTGGGTGCCATTATTGGCAAGGAG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGCCACCATCCGCAACATCACAAACAGACCCCAGTCCAAGATAGACGTGCATAGGAAG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GGCTCTCGGGGTCAG 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PNS/D) associated with breast cancer, fallopian cancer, and SCLCa and characterized primarily by loss of inhibitory control of motor neurons in the spinal cord and brainstem. Recognized by the IgG autoantibody ANNA-2 (also called anti-Ri). SIMILARITY: Contains 3 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 GlnAsnGlyThrHisThrGlyValProlleAspLeuAspProProAspSerArgLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:::::|||:::||GlnTyrPheLeuIysValLeuIleFroSerTyrAlaAlaGlySerIleIleGlyLysGly
                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00013; KH; 3. SMART; SM00322; KH; 3. PROSITE; PS50084; KH TYPE_1; 3. Antigen; Nuclear protein; RNA-binding; Repeat; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIG=VSF 002841.
Missing (in isoform 3).
/FTIG=VSP 002842.
VKIIVPNS -> KRINISWIS (in isoferm 2).
/FTIG=VSP 002843.
/FTIG=VSP 002843.
/FTIG=VSP 002844.
/FTIG=VSP 002844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KH 1.
KH 2.
ALA-RICH.
KH 3.
Missing (in isoform 2).
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68
173
161
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                      GO: GO:0003723; F:RNA binding; TAS.
GO: GO:0007626; P:locomotory behavior; TAS.
GO: GO:0008380; P:RNA splicing; TAS.
GO: GO:0007268; P:synaptic transmission; TAS.
INTERPRO; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
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EMBL; Z70771; CAA94810.1; -.
PIR; I38489; I38489.
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GK; P51513; -.
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248 23 308

ACCCAGTCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCCATC 367

43

368 AGTGTGCACTCCACCCCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATG 427

-----GCTGACGAGGTTCCC 469

:::::: | GluGluAspIleAsnSerSerMetThrAsnSerThrAlaAlaSerArgProProValThr

80

470

428 CATAAAGAGGCTAAGGACACCAAAACG-------

79

530 CTGAAGAAGGTAGAGGAAGATACCGAGACAAAATCACCATCTCCTCGTTGCAAGACCTT

100 LeuArgLeuValValProAlaThrGlnCysGlySerLeuIleGlyLysGlyGlyCysLys

138

550 GCCGAGCAGGAAATA-----ATGAAGAAAGTTCGGGAGGCCTATGAGAATGAT 158 CysValLysGlnIleCysLeuValMetLeuGluThrLeuSerGlnSerProGlnGlyArg

590 ACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGG

649

697

751 197

178 ValMetThrileProTyrGlnProMetProAlaSerSerProVallleCysAlaGlyGly

GIGGCTGCCATGAGCTCTCACCTGATCCCTGAAC-----CTGGCTGCTGTAGGT

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                                                                 1187 GAGGIGGIAGIACCAAGA-----GACCAGACCCCIGAIGAGAACGACCAGGICAICGIG 1240
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                    475
         GGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCT
                                                                               |||
|457 ArgileGlnIleSerLysiysGlyGluPheValProGlyThrArgAsnArgLys---Val
                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                   1241 AAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAA 1279
                                                                                                              ThrileThrGlyThrProAlaAlaThrGlnAlaAlaGln 488
                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1).
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Matches:
Conservative:
Mismatches:
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218.50
41.90%
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Pred. No.:
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PCB1_RABIT
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CCCGAAACACCTGCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCAA 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pro---ValGluGlySerSerGlyArgGlnValThrileThrGlySerAlaAlaSerIle 336
                          238 LeuAsnGlnValAlaArgGlnGlnSerHisPheAlaMetMetHisGlyGlyThrGlyPhe
                                                                                                                                                                                                                                                                                 839 GAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCCAGTGGGCGCCATCATCGGCAAG
                                                                                                    218 ProLeuAspAlaTyrSerIleGlnGlyGlnHisThrIleSerProLeuAspLeuAlaLys
                                                                                                                                                                                                            ---TATAGCTCCTTTATGCAGGCTCCC
 ------TTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCT
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752 CTT----
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RESULT 13 PCB4_HUMAN

356 75 75 139 69

Indels:

Score:
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Best Local S Query Match:

Gaps:

US-09-270-437D-5 (1-1708) x PCB1_RABIT (1-356)

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MEDINE-2138257; PubMed=12477932;

MEDINE-2138257; PubMed=12477932;

MALTAUSDER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Altschul S.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

Maha S.S., Loquellano N.A., Ferers G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Ferers G.J., Abramson R.D., Mullahy S.J.,

Brichards S., Worley K.C., Hales S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield V. Schein J.B., Jones S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield V. Schein J.B., Jones S.J.M., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length

Froc. Natl. Acad. Sci. US.A. 99:16899-16903(2002).

Proferentially to oligo dG (By similarity).

SIMILARITY: Contains 3 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
ISOGAL T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
ISOGAL T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takfguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninoniya K., Iwayanagi T.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20396135; PubMed=10936052;
Makeyev A.V., Liebhaber S.A.;
"Identification of two novel mammalian genes establishes a subfamily
of KH-domain RNA-binding proteins.";
Genomics 67:301-316 (2000).
                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCSI_TaxID=9606;
                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
Poly(rC)-binding protein 4 (Alpha-CP4).
403 AA
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GO, GO:0005634; C:nucleus; ISS.
GO; GO:0003677; F:DNA binding; ISS.
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EMBL, AK02393; BAB14761.1; -.
EMBL, BC003008; AAH03008.1; -.
EMBL, BC004153; AAH04153.1; -.
STANDARD;
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SEQUENCE FROM N.A.
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275 GAGGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG 334
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Lys1leLysGluIleArgGluThrThrGlyAlaGlnValGlnValAlaGly-----Asp 140
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198 GlyPheSerValGlnGlyGlnTyrGlyAlaValThrProAlaGluValThrLysLeuGln 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TCATCCAGCGCAGTCCCG---CCGCCTCCCCAGCAGCGTTACTGGGGCTGCTCCC 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ThrileSerGluGlySerCysProGluArgile
                                                                                                                                                                                                                                                                                                                                                                                             36 LysGlyGluThrValLysArglleArgGluGlnSerSerAlaArglle----
GO; GO:0003723; F:RNA binding; NAS.
GO; GO:0016071; P:RNA metabolism; ISS.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH type_1.
Pfam; PF00013; KH; 3.
SMART; SM00322; KH; 3.
SMART; SM00322; KH; 13.
PROSTIE; PSS0004; KH TYPE 1; 3.
Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding;
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880
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KH 2.
KH 3.
v; 3D99F762A9471265 C
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Mismatches:
Indels:
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Matches:
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                                                                                                                       67 KH
154 KH
293 KH
41481 MW;
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217.50
42.63%
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241
243
403 AA;
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                                                                                              GCAGTGGGCGCCATCATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCC 934
                                                AGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATC 994
                                                                                                                                                                                                                                                                                                                                                                                                           acid binding protein that binds
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20396135; PubMed=10936052;
Makeyev A.V., Liebhaber S.A.;
"Identification of two novel mammalian genes establishes a subfamily
of KH-domain RNA-binding proteins.";
Genomics 67:301-316(2000).
                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00013; KH; 3. SMART; SM00322; KH; 3. PROSITE; PS50084; KH TYPE 1; 3. Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding; Repeat.
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79
115
65
                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: Single-stranded mucleic acid binding preferentially to oligo dC (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Contains 3 KH domains.
                                                                                                                           995 ATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAG 1030
                                                                                                                                         291 IleThrGlySerProValSerIleAlaLeuAlaGln 302
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Matches:
Conservative:
Mismatches:
Indels:
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly(rC)-binding protein 4 (Alpha-CP4).
                                                                                                                                                                                                 403
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3.2.1
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InterPro; IPR004087; KH dom.
InterPro; IPR004988; KH_type_1.
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293
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101
241
403 AA;
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                           83 LeuAspGluAspLeuCysAlaAlaProAlaAsnGlyGlySerValSerArgProProval 102
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LysileLysGluileArgGluThrThrGlyAlaGinValGlnValAlaGly-----Asp 140
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198 GlyPheSerValGlnGlyGlnTyrGlyAlaValThrProAlaGluValThrLysLeuGln 217
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52 -------sprogluargile 62
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                                                                                                    36 LysGlyGluThrValLysArgIleArgGluGlnSerSerAlaArgIle-----
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                                                                                                                                                                             INCLE-MAY be due to a competing acceptor site. No experimental confirmation available; dometing acceptor site. No experimental confirmation available; dometing someting that contains 5 KH domains both domains caution. Ref. 1 sequences differ from that shown due to erroneous gene model prediction. At4918370 and At4918375 were originally fused into a single gene.
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RART; SMO322; KH; 5.
PROSITE; PS50084; KH TYPE_1; 5.
Hypothetical protein; Nuclear protein; RNA-binding; Repeat;
Alternative splicing; KH 1.
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/FIIdavSP 008899.
Missing (in isoform 2).
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w; 61F135BB8647CCC CRC64;
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105
91
201
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22
                                                                                                                                IsoId=P58223-1; Sequence=Displayed;
Note=No experimental confirmation available;
                 -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
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EMBL; AL161548; CAB78839.1; ALT_SEQ.
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EMBL, BT001108; AAN64172.1; -.
InterPro; IPR004089; KH dom.
Interpro; IPR004088; KH-type_1.
Ffam, PF00013; KH, 5.
SWART; SM00322; KH; 5.
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Science 302:842-846(2003)
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SerAspé ATCCTGG I:: LeuLeul AAGGTAG I:::: Argileé IIACAGG IIACAGG IIACAGG IIACAGG IIACAGGG IIIGIAI IIASPAAAGGG AAAACGG AAAACGG AAAACGG AAAACGG AAAACGG AAAACGG IIIIIIIIII	agaagg
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ASPAIAILEVAIA GAGGTTCCCTGA GAGCGAACCTGA GGACGGAACCTGA GIJGIUASNITEL CAGAGCCTTACCC ::: ::: ValileSerGlyG AAGAAGTTCGG- TyrLySILEASNP ATGAGC AlaSerValleASP GTGTAGGTCTTT SerValSerASPB GTGTAGGTCTTT SerValSerASPB GTGTAGGTCTTT SerValSerASPB GTGTAGGTCTCCC :::	AAGCAGG
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qq	458	458 ArgLeuArgGluAspValLeuGlyAspLysAspSerValAlaThrArgLys	474
ò	1367	1367 GCCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACGGGCAGAATCGAGAGTGT 1420	1420
Ob	475	 475ProProAlaArgThrAspAsnCysSerPheLeuSerGlySerSerAsnAlaGlyTyr 493	493
ģ	1421	1421 GCTCTCCCCGGC 1432	1432
Db	494	494 ThrLeuProSerPheMetSerSerMetAlaSerThrSerGlyPheHisGlyTyrGlySer 513	513
ò	1433	1433 AGGCCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGGGCTGTAGATCAGGTTTGCCC 1492	1492
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